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Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                        Result
                                                                                                                                                                                                                                                                                                                                  Database
                                                                                                                                                                                                                                                                                                                                                                              Minimum DB
Maximum DB
                                                                                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                         Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein -
                                                                                                                                                                                                                                   No.
 hed:
                                                                                                                                                                                                                                                                                     Pred. No.
                                                                                                                                                                                                                                   Score
                                                                                                                                                                                                                                                                     d. No. is the number of results predicted by chance to have a
re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                             seq
 protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                             length: 0
length: 2000000000
Match
                                                                                                                                                                                                                                                                                                                                  PIR_68:*
                                                                                                                                                                                                                                                                                                                                                                                                                                 BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-692-401-5
50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    June 20, 2001, 14:04:33; Search time 28.81 Seconds (without alignments) 26.440 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                Maximum Match 100%
Listing first 45 s
                                                                                                                                                                                                                                                                                                                                                                                                                   219241 segs, 76174552 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd
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CDP-diacylglycerol
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protein F23N19.5
                                                                                                                                                                                                                                  Description
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                                                                                                                                                                    probable membrane
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ethylene.
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| 45 | 44 | 43 | 42 | 41 | 40 | 39 | 38 | 37 | 36 | 35 | 34 | 33 | 32 | 31 | 30 |
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| 32 | 32 | 32 | 32 | 32 | 32 | 32 | 32 | 32 | 32 | 32 | 33 | ω ω | 33 | 33 | 33 |
| 64.0 | 64.0 | 64.0 | 64.0 | 64.0 | 64.0 | 64.0 | 64.0 | 64.0 | 64.0 | 64.0 | 66.0 | 66.0 | 66.0 | 66.0 | 66.0 |
| 449 | 415 | 379 | 368 | 354 | 350 | 321 | 256 | 256 | 252 | 191 | 1232 | 1112 | 663 | 619 | 538 |
| 2 | 2 | ب | 2 | 2 | 2 | N | N | N | ب | 2 | 2 | N | Ν | ب | L |
| T29366 | S43484 | C70124 | JC6081 | T04779 | E72352 | F84611 | JQ1106 | S26742 | н69002 | H84544 | T06165 | D75056 | A75461 | S48729 | QQECD7 |
| hypothetical prote | heterogeneous nucl | conserved hypothet | proximal sequence | hypothetical prote | N-acetylglucosamin | hypothetical prote | tonoplast intrinsi | tonoplast intrinsi | conserved hypothet | hypothetical prote | multidrug resistan | cell division cont | DNA gyrase, subuni | glucokinase regula | tnsE protein - Esc |

ALIGNMENTS

N;Alternate names: MAGE 21 protein C;Species:.Homo sapiens (man) C;Dapte: 07-Jun-1996 #§sequence_revision 07-Jun-1996 #text_change 18-Feb-2000 C;Acceasion: I54519; JC2362; PHI295 R;De Smet, C;; Lurquin, C;; van der Bruggen, P.; De Plaen, E.; Brasseur, F.

H

melanoma antigen MAGE-12 - human

RESULT 154519

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Immunogenetics 39, 121-129, 1994.

A;Title: Sequence and expression pattern of the human MAGE2 gene.

A;Reference number: 154519; MUID:94102805

A;Status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A:Molecule type: mRNA, R;Residues: 1-9,'S',11-186,'D',188-299,'S',301-314 <DIN>A;Residues: 1-9,'S',11-186,'D',188-299,'S',301-314 <DIN>A;Experimental source: melanoma cell line DM150; MAGE-12f R:Traversari, C.; van der Bruggen, P.; Luescher, I.F.; Lurquin, C.; Chomez, P.; Van P. J. Exp. Med. 176, 1453-1457, 1992
A;Trile: A nonapptide encoded by human gene MAGE-1 is recognized on HLA-A1 by cytoly A;Reference number: PH1294; MUID:93018875
A;Accession: PH1295
                        RESULT
B96652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:L18877; NID:g499345; PIDN:AAA19023.1; PID:g499346 R;Ding, M.; Beck, R.J.; Keller, C.J.; Penton, R.G. Biochem. Biophys. Res. Commun. 202, 549-555, 1994 A;Title: Cloning and analysis of MAGE-1-related genes.
A;Reference number: JC2358; MUID:94311935
A;Accession: JC2362
                                                                                                                  Вр
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C;Superfamily: tumor associated protein MAGE
F;168-176/Region: HLA-Al binding #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                    A; Cross-references: GDB:331129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 168-176 < TRA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-314 <DES>
protein F23N19.5 [imported] - Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Experimental source: MAGE-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                            Matches
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Best Local
                                                                                                                  169
                                                                                                                                                               1 VVRIGHLYIL 10
                                                 N
                                                                                                               VVRIGHLYIL 178
                                                                                                                                                                                                              10;
                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                  100.0%;
                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                  Score 50; DB 2
Pred. No. 0.02;
                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                        DB 2; Length 314;
                                                                                                                                                                                                              0;
                                                                                                                                                                                                              Indels
                                                                                                                                                                                                              0
                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                              0;
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: B96652
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Liu, X.; Liu, S.X.; Liu, Z.A.; Liu, S.X.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Accession: B96652
A;Accession: B96652
A;Accession: Present Company of the plant Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:L18920; NID:g436180; PIDN:AAA17729.1; PID:g436181 R;Traversari, C.; van der Bruggen, P.; Luescher, I.F.; Lurquin, C.; Chomez, J. Exp. Med. 176, 1453-1457, 1992 Aprile: A nonapeptide encoded by human gene MAGE-1 is recognized on HLA-Al a Prence number: PH1294; MUID:93018875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  melanoma antigen MAGE-2 - human
C;Species: Homo sapiens (man)
C;Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 18-Feb-2000
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A; Residues: 1-233 <S
RESULT
G85255
                                                                                            В
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                                                                                                                                                                   Query Match
Best Local Similarity
"hes 8; Conserv?
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A;Cross-references: GDB:273684
A;Map position: Xq28 Xq28
C;Superfamily: tumor associated protein MAGE
                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 168-176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-314 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Title: Sequence and expression pattern of the human MAGE2 gene A;Reference number: I54519; MUID:94102805
A;Accession: I68889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;De Smet, C.; Lurquin, C.; van der Bruggen, P.; De Plaen, Immunogenetics 39, 121-129, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Accession: 168889; PH1294
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                                                                                                                                                                                                                                                                                                                                                                                                      Genetics
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                                                                                            169 VVPISHLYIL 178
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                                                                                                                                                                                                                                                                                                                                                                                                                            <TRA>
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                                                                                                                                                                                       Score 37; DB 2
Pred. No. 8.3;
0; Mismatches
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3.7;
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                                                                                                                                                                                                                                     Length 314;
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CDP-diacylglycerol synthetase-like protein [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Feb-2001 C;Accession: G8525 R;Anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Rature 402, 769-777, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Map position: 4
A; Introns: 25/3; 110/2; 161/1; 208/2; 260/3; 276/3; 305/3; 348/3; 367/3; 395/3
A; Note: T10I14.170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDP-diacylglycerol synthetase homolog T10I14.170 - Arabidopsis thaliana (fragment) C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-Jun-1999 C;Accession: T04915
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Best Local Similarity
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A; Accession: T04915
A; Molecule type: DNA
A; Residues: 1-423 <BEV>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, submitted to the Protein Sequence Database, April 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Map position:
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A; Residues: 1-423 <STO>
                                                                                                                                                                                                                           CDP-diacylglycerol synthetase homolog F2401.17 - Arabidopsis thaliana C:Species: Arabidopsis thaliana (mouse-ear cress) C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 23-Mar-2001 C:Accession: T01455
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
                                      A, Status: translated from GB/EMBL/DDBJ
A, Molecule type: DNA
A, Residues: 1-427 <SHI>
                                                                                                                                                                                                                                                                                                                                                                                               Дb
                                                                                                                                                                                                                                                                                                                                                                                                                                    δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: EMBL:AL021712
A;Experimental source: cultivar Co
                                                                                                       A; Reference number: A; Accession: T01455
                                                                                                                            A; Description: Genomic sequence A; Reference number: Z14211
                                                                                                                                              submitted to the EMBL Data Library, January 1998 A; Description: Genomic sequence for Arabidopsis
                                                                                                                                                                                    R;Shinn, P.; Buehler, eologis, A.; Ecker, J.
                       A;Cross-references:
                                                                                                                                                                                                                                                                                                                                     RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gene: AT4g22340
Map position: 4
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6; Conserv
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nces: EMBL:AC003113; NID:g2689438; PID:g2781361
Source: cultivar Columbia
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                                                                                                                                                                                                        E.; Dewar,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cultivar Columbia; BAC clone T10I14
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Pred. No. 18;
2; Mismatches
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Pred. No.
                                                                                                                                                                                                              K.; Feng, J.; Kim,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2;
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                                                                                                                                                                                                              Li, Y.; Sun, H.; Conway,
                                                                                                                                                    BAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
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C;Genetics:
A;Map position: 1
A;Introns: 25/3; 110/2; 161/1; 208/2; 260/3; 276/3; 305/3; 348/3; 373/3; 401/3
A;Note: F2401.17
                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-305 <RES>
A;Cross-references: EMBL:U32380; NID:g1049123; PIDN:AAC44422.1; PID:g1049128
A;Experimental source: plasmid pTA1060
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic Acids Res. 23, 612-619, 1995
A;Title: Characterization of single strand
A;Reference number: 140549; MUID:95206941
A;Accession: 140565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
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A; Residues: 1-234 <HAR>
A; Cross-references: EMBL: AL109972;
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C;Superfamily:
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A; Accession: T37141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A. submitted to the EMBL Data Library, August 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Meijer, W.J.; Venema,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pothetical protein 4.60 - Bacillus subtilis plasmid pTA1060 Species: Bacillus subtilis Date: 12-Aug-1996 #sequence revision 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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pecies: Streptomyces coelicolor
   197
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mes 7; Conser
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03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 VVRIGHLYI 9
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   VLIGHVYVL 205
                                                            VRIGHLYIL 10
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77.8%;
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                                                                                                                        Score 35; DB
Pred. No. 20;
2; Mismatches
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Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ore 36; DB
ed. No. 18;
Mismatches
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R; Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Ber C.; Bron, S.; Brouillet, S.D.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Febret, C.; Ferrari, Nature 390, 249-256, 1997

A; Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galicch, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M. Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino A; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mau y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portete Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanl A; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Se akeuchi, M.; Tamakoshi, A.; Tananoto, H.; Yamamoto, H.; Yamamoto, K.; Yasumoto, K.; Yata, K.; Yoshida A; Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A, Title: The complete genome sequence of the Gram positive bacterium Bacillus subtili A.; Reference number: A69580; MUID:98044033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein yopk - Bacillus subtilis phage SPBc2 C; Species: Bacillus subtilis phage SPBc2 C; Species: Bacillus subtilis phage SPBc2 C; Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 20-Jun-2000 C; Accession: T12852; H69917 R; Lazarevic, V.; Duesterhoeft, A.; Soldo, B.; Hilbert, H.; Mauel, C.; Karamata, submitted to the EMBL Data Library, August 1997 A; Description: The complete nucleotide sequence of the Bacillus subtilis SPbetack, Reference number: Z17583
                                                                                                                                                                                         \begin{array}{lll} \textbf{A}; \textbf{Gene: yopR} \\ \textbf{C}; \textbf{Superfamily: Bacillus subtilis phage SPBc2 hypothetical protein} \end{array}
                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-325 < KUN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                          A; Experimental source: strain
                                                                                                                                                                                                                                                                                                                                                                      A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: EMBL:AF020713; NID:g3025478; PID:g3025566; PIDN:AAC13061.1
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                                                                                                                                                                                                                                                                                    Genetics:
                                      Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      acid sequence not shown;
                                                                                                                                                                                                                                                                                                                               GB:Z99114; GB:Z99115;
ce: strain 168
                                      70.0%;
Score 35; DB
Pred. No. 22;
1; Mismatches
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                                                                                 Length 325
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cytochrome P450 (EC 1.14...) 81Blc - Jerusalem artichoke C;Species: Helianthus tuberosus (Jerusalem artichoke) C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Feb-2001 C;Accession: T10896
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-505 <CAB>
                                                                                                                                             R;Cabello-Hurtado, F.; Batard, Y.; Salaun, J.; Durst, F.; Pinot, F.; Werck-Reichhart, J. Blol. Chem. 273, 7260-7267, 1998
A;Title: Cloning, expression in yeast and functional characterization of CYP81B1, a p A;Reference number: Z17204; MUID:98184826
                                                                                                       A; Reference number: A; Accession: T10896
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밁 QΥ

Matches

Local Similarity hes 6; Conser 1 WRIGHLY 8

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A;Description: specifically catalyzes the hydroxylation of medium chain saturated fat C;Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homology C;Keywords: chromoprotein; fatty acid metabolism; heme; iron; metalloprotein; oxidore

A; Cross-references: EMBL:A: A; Experimental source: cv.

EMBL:AJ000477; NID:g3059128; PIDN:CAA04116.1;

PID:g3059129

C; Genetics:

A; Gene:

Function

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Query Match
Best Local Similarity
6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GcpE protein [imported] - Chlamydophila pneumoniae (strain J138)
C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Mar-2001
C;Accession: C86537
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A;Gene: gcp
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A-Title: Comparison of whole genome sequences of chlamydia efference number: A86491; MUID:20330349
Accession: C86537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F;301-463/Domain: cytochrome P450 homology <P45>
F;441/Binding site: heme iron (Cys) (axial ligand) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                 gcpE protein CP0383 [imported] - Chlamydophila pneumoniae (strains CWL029 and
C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-May-2000
C;Accession: E72087; D81582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:BA000008; NID:g8978745; PIDN:BAA98581.1; A;Experimental source: strain J138
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A; Residues: 1-613 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              В
                                                                                    A;Cross-references: GB:AE002200; GB:AE002161; A;Experimental source: strain AR39, HL cells C;Genetics:
                                                                                                                                                                        Nucleic Acids Res. 28, 1397-1406, 2000
A;Title: Genome sequences of Chlamydia trachomatis A;Reference number: A81500; MUID:20150255
A;Accession: D81582
                                                                                                                                                                                                                                                                                                                                                                                                   R; Kalman, S.; Mitchell, W.; Marathe, R.; Nature Genet. 21, 385-389, 1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R; Shirai, M.; Hirakawa, H.; Kimoto,
                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-613 < REA>
                                                                                                                                                                                                                                           A; Experimental source: strain CWL029
R; Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.;
C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.
                                                                                                                                                                                                                                                                                             A;Molecule type: DNA
A;Residues: 1-613 <ARN>
A;Cross_references: GB:AE001621; GB:AE001363; NID:g4376641; PIDN:AAD18517.1; PID:g43766
                                                                    A;Gene:
Query Match
Best Local
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Best Local
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                                                                                                                                                                                                                                                                                                                                              tle: Comparative genomes of Clamydia pneumoniae ference number: A72000; MUID:99206606 session: E72087
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Local Similarity
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                                                                  gcpE; CP0383
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85.7%;
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   70.0%;
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Pred. No. 44;
1; Mismatches
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Pred. No. 35;
1; Mismatches
   Score
Pred.
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   35;
No.
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35;
 DB
44;
                                                                                                                         NID: 97189305; PIDN: AAF38230.1;
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                   Length
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                       613;
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                                                                                                                                                                                                                                                  J.; McClarty,
                                                                                                                                                                                                                                                                  J.F.;
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                                                                                                                                                                                                                                                                  White,
                                                                                                                                                                                                                                                  G.;
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R;Cole, S.T., Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; H.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.; Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the comple A;Reference number: A70500; MUID:98295987
A;Accession: H70535
                                                                                                                                           A; Nolecule type: DNA
A; Nolecule type: DNA
A; Residues: 1-481, 'RT', 484-728 <SE2>
A; Residues: 1-481, 'RT', 484-728 <SE2>
A; Residues: 1.481, 'RT', 484-728 <SE2>
A; Riddener, K. M.; Arakaki, N.; Hartmann, G.; Vandekerckhove, J.; Weingart, S.; Rieder, R.; Weingart, S.; Rieder, B.; Proc. Natl. Acad. Sci. U.S.A. 88, 7001-7005, 1991
A; Title: Evidence for the identity of human scatter factor and human hepatocyte growth approximate number: A41140; MUID:91334393
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C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: DDBJ:D90318
A;Note: the authors translated the codon GAA for residue 662 as Gly
R;Seki, T.; Hagiya, M.; Shimonishi, M.; Nakamura, T.; Shimizu, S.
submitted to JIPID, March 1991
A;Description: Organization of the human hepatocyte growth factor-encoding gene.
A;Reference number: JU0333
A;Accession: JU0333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Homo sapiens (man)
C;Date: 17-Aug-1992 #sequence_revision 17-Aug-1992 #text_change 08-Dec-2000
C;Date: 17-Aug-1993 #sequence_revision 17-Aug-1992 #text_change 08-Dec-2000
C;Accession: JH0579; JU0333; A41140; B36677; A36677; A33512; A39006; PH0114;
C;Accession: JH0579; JU0333; A41140; B36677; A36677; A33512; A39006; PH0114;
R;Seki, T; Hagiya, M; Shimonishi, M.; Nakamura, T; Shimizu, S.
Gene 102, 213-219, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Superfamily: Mycobacterium tuberculosis hypothetical protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Gene: Rv0669c
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A; Residues: 1-637 <COL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Status: preliminary; nucleic acid sequence
A;Cross-references: GB:M73239; NID:g337935; PIDN:AAA64239.1; PID:g337936 R;Seki, T.; Thara, I.; Sugimura, A.; Shimonishi, M.; Nishizawa, T.; Asam Biochem. Biophys. Res. Commun. 172, 321-327, 1990
                                                                                            A; Molecule type: mRNA
A; Residues: 1-728 <WEI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-728 <SEK>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hepatocyte growth factor precursor [validated] - human
N;Alternate names: hepapoletin A; scatter factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Accession: JH057
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Best Local S
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Pred. No.
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46;
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                                         T.; Asami,
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                                               O.; Hagiya
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A; Note: the authors translated the codon CAG for residue 727 as Glu A; Note: part of this sequence, including the amino end of both the alpha and R; Hartmann, G.; Naldini, L.; Weidner, K.M.; Sachs, M.; Vigna, E.; Comoglio, P Proc. Natl. Acad. Sci. U.S.A. 89, 11574-11578, 1992
A; Title: A functional domain in the heavy chain of scatter factor/hepatocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Accession: A37/yo
A;Molecule type: protein
A;Molecule type: protein
A;Residues: 86-91;329-344;356-363,'XX',366-370;425-434;442-447,'X',449-450;543-546,
A;Residues: 87-13-27, Nishizawa, T.; Hagiya, M.; Seki, T.; Shimonishi, M.; Sugimura, A.; 'R.Nakamura, T.; Nishizawa, T.; Hagiya, M.; Seki, T.; Shimonishi, M.; Sugimura, A.; 'R.Nakamura, T.; Nishizawa, T.; Hagiya, M.; Seki, T.; Shimonishi, M.; Sugimura, A.; 'R.Nakamura, T.; Nishizawa, T.; Hagiya, M.; Seki, T.; Shimonishi, M.; Sugimura, A.; 'R.Nakamura, T.; Nishizawa, T.; Hagiya, M.; Seki, T.; Shimonishi, M.; Sugimura, A.; 'R.Nakamura, T.; Nishizawa, T.; Hagiya, M.; Seki, T.; Shimonishi, M.; Sugimura, A.; 'R.Nakamura, T.; Nishizawa, T.; Hagiya, M.; Seki, T.; Shimonishi, M.; Sugimura, A.; 'R.Nakamura, T.; Nishizawa, T.; Hagiya, M.; Seki, T.; Shimonishi, M.; Sugimura, A.; 'R.Nakamura, T.; Nishizawa, T.; Hagiya, M.; Seki, T.; Shimonishi, M.; Sugimura, A.; 'R.Nakamura, T.; Nishizawa, T.; Hagiya, M.; Seki, T.; Shimonishi, M.; Sugimura, A.; 'R.Nakamura, T.; Nishizawa, T.; Hagiya, M.; Seki, T.; Shimonishi, M.; Sugimura, A.; 'R.Nakamura, T.; Hagiya, M.; Seki, T.; Shimonishi, M.; Sugimura, A.; 'R.Nakamura, T.; Hagiya, M.; Seki, T.; Shimonishi, M.; Sugimura, A.; 'R.Nakamura, T.; Hagiya, M.; Seki, T.; Shimonishi, M.; Sugimura, A.; 'R.Nakamura, T.; Hagiya, M.; 'R.Nakamura, T.; 'R.Nakamura, 
                                                                                                                                                                      A;Title: An alternatively processed mRNA generated A;Reference number: S15443; MUID:91200041
A;Accession: S15443
                                                                                                                                                                                                                                                                                                                                                                                                            A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-288,'ET' <HAR>
                                                                                                                                                                                                                                                                                           A;Cross-references: GB:L02931; NID:g184033; PIDN:AAA52649.1; R;M1yazawa, K.; Kitamura, A.; Naka, D.; Kitamura, N. Eur. J. Blochem. 197, 15-22, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Reference number: A; Accession: I59214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,Experimental source: embryonic lung
R;Yoshiyama, Y.; Arakaki, N.; Naka, D.; Takahashi, K.; Hirono, S.; Kondo, J.;
Biochem. Biophys. Res. Commun. 175, 660-667, 1991
A,Title: Identification of the N-terminal residue of the heavy chain of both
A;Reference number: PH0114; MUID:91207365
A;Recession: PH0114
A;Molecule type: protein
A;Residues: 32-43;53-58 <70S>
A;Residues: 32-43;53-58 <70S>
A;Experimental source: plasma
R;Weidher, K.M.; Behrens, J.; Vandekerckhove, J.; Birchmeier, W.
J. Cell Blol. 111, 2097-2108, 1990
A;Title: Scatter factor: molecular characteristics and effect on the invasive
A;Reference number: A37796; MUID:91035621
                         A; Cross-references:
                                                      A; Molecule type: mRNA
A; Residues: 1-288, 'ET' <MIY2>
                                                                                                                                         A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: mRNA
A;Residues: 1-31,'HK',34-77,'N',79-292,'V',294-299,'M',301-316,'A',318-335,'K',337-386,
A;Cross-references: EMBL:X16323; NID:g32081; PIDN:CAA34387.1; PID:g32082
A;Experimental source: liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               itle: Molecular cloning and expression of human Reference number: S06794; MUID:90066676
A:Accession: S06794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A7Cross-references: GB:M29145; NID:g184041; PIDN:AAA52650.1; PID:g306846 R;Rubin, J.S.; Chan, A.M.L.; Bottaro, D.P.; Burgess, W.H.; Taylor, W.G.; Proc. Natl. Acad. Sci. U.S.A. 88, 415-419, 1991 A;Title: A broad-spectrum human lung fibroblast-derived mitogen is a vari A;Reference number: A39006; MUID:91110540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Experimental source: leukocyte R;Miyazawa, K.; Tsubouchi, H.; Naka, D.; Takahashi, K.; CR;Miyazawa, K.; Tsubouchi, H.; Naka, D.; Takahashi, K.; CB;Diochen. Biophys. Res. Commun. 163, 967-973, 1989 A;Title: Molecular cloning and sequence analysis of cDNA A;Reference number: A33512; MUID:89392017 A;Accession: A33512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-161,167-728 < RUB>
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A;Accession: A36677
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A: Residues: 1-728 <SE3>
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sidues: 1-728 <MIY>
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                    EMBL: X57574;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               I59214; MUID:93087571
            NID: 932083; PIDN: CAA40802.1;
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            PID: g32084
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P.M.;
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                                                                           A;Residues: 1-728 <OKA>
A;Cross-references: EMBL:X54400; NID:g56353; PIDN:CAA38266.1; PID:g4539554
Crommlex: disulfide-bonded heterodimer of chains derived from the same pr
                                                                                                                                                                                                                                                                                                                                                                                                                             A; Status: Frank
A; Molecule type: mRNA
A; Residues: 1-728 <TAS>
A; Residues: 1-728 <TAS>
A; Cross references: GB:D90102; GB:M32987; NID:9220766; PIDN:BAA14133.1;
A; Note: the authors translated the codon GAG for residue 70 as Gln, GAC
A; Note: the authors translated the codon GAG for residue 70 as Gln, GAC
                                                                                                                                                                                                                                                                                                            R;Okajima, A.; Miyazawa, K.; Kitamura, N.
Eur. J. Biochem. 193, 375-381, 1990
A;Title: Primary structure of rat hepatocyte
A;Reference number: S13211; MUID:91031482
A;Accession: S13211
                                         A; Description:
                                                                                                                                                                                                                                     A; Molecule type: mRNA
                                                                                                                                                                                                                                                                           A; Status: preliminary
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Biochem.
A;Title:
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A; Residues: 161-166 <:
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                                         stimulates
    have
proteinase
                                         mitosis
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F:128-206/Domain: kringle homology <KR1>
F:211-288/Domain: kringle homology <KR2>
F:305-383/Domain: kringle homology <KR3>
F:391-469/Domain: kringle homology <KR4>
F:495-728/Domain: beta chain #status experimental <BCH>
F:495-728/Domain: trypsin homology <TRY>
F:495-716/Domain: trypsin homology <TRY>
                                                                                                                                  F;32/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) F;294,402,566,653/Binding site: carbohydrate (Asn) (covalent) #status F;487-604/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                          F;1-31/Domain: signal sequence #status predicted <SIG>
F;32-494,495-728/Product: hepatocyte growth factor #status experimental
F;32-494/Domain: alpha chain #status experimental <ACH>
F:32-494/Domain: alpha chain #status experimental <ACH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Note: does not have proteinase activity
C; Superfamily: hepatocyte growth factor; kringle homology; trypsin homology
C; Keywords: alternative splicing; glycoprotein; growth factor; heterodimer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GDB:127524; OMIM:142409
A;Map position: 7g21.1-7g21.1
A;Introns: 30/1; 85/2; 123/1; 161/2; 209/1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross~references: GB:S62561; NID:g237996; PIDN:AAB20169.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Complex: disulfide-bonded heterodimer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biophys. Res. Commun. ***, **** growth factor Tumor cytotoxic factor/hepatocyte growth factor number: I52253; MUID:92062058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N.; Nagao, M.; Ogaki, F.; Tsuda, E.; 1
Biophys. Res. Commun. 180, 1151-1158,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             preliminary; translated from GB/EMBL/DDBJ
  Similarity 50.05; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             stimulates mitosis of hepatocytes and other cells
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                                70.0%;
                          Score 35;
Pred. No. 5
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Gaps
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R;Tashiro, K.; Hagiya, M.; Nishizawa, T.; Seki, T.; Shimonishi, M.; Shimizu, Proc. Natl. Acad. Sci. U.S.A. 87, 3200-3204, 1990
A;Title: Deduced primary structure of rat hepatocyte growth factor and expres A;Reference number: A35644; MUID:90222197 hepatocyte growth factor precursor - rat
N:Alternate names: hepapoietin A; scatter factor
C;Species: Rattus norvegicus (Norway rat)
C;Date: 28-Sep-1990 #sequence_revision 18-Nov-1992 #text_change 21-Jul-2000 A35644; S13211 expression of s.;

of hepatocytes activity

and

precursor

and

induction

PID: g220767 for

residue

OM protein - protein search, using sw model GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

June 20, 2001, 14:04:34; Search time 28.81 Seconds (without alignments) 21.152 Million cell updates/sec

Title: Perfect score: US-09-692-401-6 1 RIGHLYIL 8

Run on:

Scoring table:

Searched:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters:

219241

219241 seqs, 76174552 residues

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_68:*

Database : pir1:*
pir2:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result

| Result | Score | Query Match | Length | DB | Ħ | Description |
|----------|-------------|----------------|--------|-----|--------|--------------------|
| ш | 42 | 100.0 | 314 | 2 : | 154519 | melanoma antigen M |
| 2 | 35 | 83.3 | 505 | Ν | 9 | me P450 (|
| w | 34 | 81.0 | 234 | N | T37141 | embrane |
| 4 | 34 | 81.0 | 1244 | ω | T01956 | hypothetical prote |
| ທ | 34 | | 1461 | 2 | E84589 | H |
| 6 | ω | 78.6 | 305 | N | I40565 | hypothetical prote |
| 7 | u u | 8 | 314 | ผ | JC2361 | ۳. |
| 00 | ω ω | 8 | 619 | Н | S48729 | glucokinase regula |
| , | i w | . 00 | 728 | ш | JH0579 | |
| 10 | i ta | . 00 | 728 | ш | A35644 | |
| <u>.</u> | ب ا ا | 78.6 | 728 | , 1 | A60185 | |
| 12 | ى ر د د | 'nċ | 000 |) (| E/2332 | N-acetylglucosamin |
| 14 | ω (2) | د د | 449 | ۱ د | STEDEL | |
| 15 | 31 | | 101 | N | E82849 | conserved hypothet |
| 16 | 31 | | 233 | N | B96652 | protein F23N19.5 |
| 17 | 31 | Ψ | 276 | N | T12552 | hypothetical prote |
| 18 | 31 | | 314 | N | I68889 | |
| 19 | 31 | Ψ | 423 | N | G85255 | ylqlyčero |
| 20 | 31 | ٠ | 423 | 2 | T04915 | CDP-diacylqlycerol |
| 21 | 31 | | 465 | N | C70594 | probable phosphoma |
| 0 10 | 31 | 73.8 | 484 | N | C84955 | UDP-N-acetylmurama |
| 2 6 | 31 | | 497 | N | JE0275 | voltage-gated pota |
| 4.1 | 1 | | 534 | N | T27054 | |
|) N | 14 | W | 537 | 2 | H84642 | |
| 20 | Į. | | 543 | N | H81102 | conserved hypothet |
| 27 | 31 | | 543 | N | F81838 | hypothetical prote |
| 28 | 31 | | 599 | N | D70104 | DNA topoisomerase |
| 29 | 31 | 73.8 | 613 | N | C86537 | GcpE protein [impo |
| | | | | | | |

RESULT T10896

N

cytochrome P450 (EC 1.14.-.-) 81B1c - Jerusalem artichoke

B

Conservative

0;

Mismatches

0;

Indels

0;

Gaps

0;

| 45 | 44 | 43 | 42 | 41 | 40 | 39 | æ | 37 | 36 | i (u) | 34 | i w | 32 | 12 | 30 |
|--------------------|--------------------|--------|--------------------|--------------------|--------------------|--------------------|--------------------|--------|--------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| 30 | 30 | 30 | 30 | 30 | 30 | 30 | 30 | 30 | 30 | 30 | ω | <u>ω</u> | ω 1 | ω | 31 |
| 71.4 | 71.4 | 71.4 | 71.4 | 71.4 | 71.4 | 71.4 | 71.4 | 71.4 | 71.4 | 71.4 | 73.8 | 73.8 | 73.8 | 73.8 | 73.8 |
| 303 | 288 | 280 | 256 | 256 | 247 | 189 | 188 | 184 | 144 | 65 | 1530 | 1507 | 720 | 615 | 613 |
| N | N | N | N | N | N | N | Ν | N | N | N | N | ν | Ν | 2 | Ν |
| C32252 | G64000 | A75614 | JQ1106 | S26742 | S67685 | A83573 | T38223 | T36644 | G70023 | A23783 | I45944 | A40228 | E82384 | C75278 | E72087 |
| gene V protein - A | hypothetical prote | | tonoplast intrinsi | tonoplast intrinsi | hypothetical prote | conserved hypothet | probable adenine p | | | hypothetical prote | neurexin I-alpha - | neurexin I-alpha p | ornithine decarbox | DNA polymerase III | gcpE protein CP036 |

ALIGNMENTS

Query Match
Best Local Similarity
"~+~hes 8; Conserva A;Gene: GDB:MAGEA12; MAGE12; MAGE-12f
A;Cross-references: GDB:331129
A;Map position: xq28-xq28
C;Superfamily: tumor associated protein MAGE
F;168-176/Region: HLA-Al binding #status predicted A;Accession: JC2362
A;Molecule type: mRNA
A;Residues: 1-9, 'S', 11-186,'D',188-299,'S',301-314 <DIN>
A;Experimental source: melanoma cell line DM150; MAGE-12f
R;Traversari, C.; van der Bruggen, P.; Luescher, I.F.; Lurquin, C.; Chomez, P.; Van P
J. Exp. Med. 176, 1453-1457, 1992
A;Title: A nonapeptide encoded by human gene MAGE-1 is recognized on HLA-Al by cytoly
A;Reference number: PH1294; MUID:93018875 A;Accession: PH1295 A;Molecule type: DNA A;Residues: 168-176 <TRA> C; Genetics: A; Experimental source: MAGE-21 A;Cross-references: GB:L18877; NID:g499345; PIDN:AAA19023.1; PID:g499346 R;Ding, M.; Beck, R.J.; Keller, C.J.; Fenton, R.G. Biochem. Biophys. Res. Commun. 202, 549-555, 1994 A;Title: Cloning and analysis of MAGE-1-related genes. A;Reference number: JC2358; MUID:94311935 R;De Smet, C.; Lurquin, C.; van der Bruggen, P.; De Plaen, E.; Brasseur, F.; Boon, Immunogenetics 39, 121-129, 1994
A;Title: Sequence and expression pattern of the human MAGE2 gene.
A;Reference number: I54519; MUID:94102805
A;Recession: I54519 C;Species: Homo sapiens (man)
C;Date: 07-Jun-1996 #sequence_revision(07-Jun-1996\#text_change 18-Feb-2000
C;Accession: I54519; JC2362; PH1295 melanoma antigen MAGE-12 - human N;Alternate names: MAGE 21 protein A; Residues: 1-314 <DES> A;Molecule type: DNA A;Status: preliminary; translated from GB/EMBL/DDBJ 100.0%; Score 42; DB 2; Length 314; 100.0%; Pred. No. 0.39; 7

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C;Species: Helianthus tuberosus (Jerusalem artichoke)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Feb-2001
C;Accession: T10896
R;Cabello-Hurtado, F.; Batard, Y.; Salaun, J.; Durst, F.; Pinot, F.; Werck-Reichhart, D.
J. Biol. Chem. 273, 7260-7267, 1998
A;Title: Cloning, expression in yeast and functional characterization of CYP81B1, a plan
A;Reference number: Z17204; MUID:98184826
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-505 <CAB>
A;Cross-references: EMBL:AJ000477; NID:g3059128; PIDN:CAA04116.1; PID:g3059129
A;Cross-references: EMBL:AJ000477; NID:g3059128; PIDN:CAA04116.1; PID:g3059129
A;Experimental source: cv. blanc commun
C;Genetics:
A;Gene: CYP81B1C
C;Function:
A;Description: specifically catalyzes the hydroxylation of medium chain saturated fatty
C;Superfamily: human cytochrome P450 romology cytochrome P450 homology
C;Keywords: chromoprotein; fatty acid metabolism; heme; iron; metalloprotein; oxidoreduc
F;301-465/Domain: cytochrome P450 homology <P45>
F;441/Binding site: heme iron (Cys) (axial ligand) #status predicted
                                                                                         hypothetical protein T2L5.9 - Arabidopsis thaliana (;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 26-Feb-1999 #sequence_revision 26-Feb-1999 C;Accession: T01956 R;Geisel, C.; Smith, A.; Le, T. submitted to the EMBL Data Library, October 1998 A;Description: The sequence of A. thaliana T2L5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Streptomyces coelicolor
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C;Accession: T37141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-234 <HAR>
A; Cross-references: EMBI
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A; Accession: T37141
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  A; Status: t
A; Molecule
                                              A; Reference number: A; Accession: T01956
                                                                    A; Description: The sequence of A; Reference number: Z14470
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Best Local :
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translated from type: DNA
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71.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 34;
Pred. No.
2; Mismatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIDN:CAB53266.1; GSPDB:GN00070; SCOEDB:SCJ9A.05c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ll, J.; Barrell, B.G.;
August 1999
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       Query Match
Best Local Similarity
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A;Residues: 1-1244 <GEI>A;Cross-references: EMBL:AF096371; NID:g3695386; A;Experimental source: cultivar Columbia C;Genetics:
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R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tall euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Ver Nature 402, 751-768, 1999

Nature 402, 751-768, 1999
                                                                                                                                                                                                                                                                                                           hypothetical protein 4.60 - Bacillus subtilis plasmid pTA1060 C; Species: Bacillus subtilis C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_chan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Gene: At2g20460
A;Map position: 2
C;Superfamily: retrovirus-related polyprotein
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
C;Accession: E04589
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A; Introns: 75/1;
A; Note: T2L5.9
A; Genome: plas
C; Superfamily:
                                                                                                                                                                         A;Title: Characterization of single strand origins of cryptic rolling-circle A;Reference number: I40549; MUID:95206941
A;Accession: I40565
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Best Local Similarity
Than 6; Conserve
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A;Residues: 1-1461 <STO>
A;Cross-references: GB:AE002093; NID:g4586028; PIDN:AAD25646.1;
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A;Accession: E84589
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana
                                                                                                                                                                                                                                                                                      C; Accession: I40565
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                                                                 A; Experimental source:
                                                                                        A; Cross-references:
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A; Residues: 1-305 < RES>
                                                                                                                                                       A;Status: preliminary;
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Bacillus subtilis plasmid pTA1060 hypothetical protein
                                                                                                                                                                                                                                               Venema, G.; Bron, S.
es. 23, 612-619, 1995
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                                                                 EMBL:U32380; NID:g1049123; PIDN:AAC44422.1; PID:g1049128
>e: plasmid pTA1060
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Pred. No. 83;
2; Mismatches
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Pred. No. 1e+02;
2; Mismatches
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83;
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C. Y

78.6%; 71.4%;

Score Pred. No.

DB 28;

2;

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melanoma antigen MAGE-3 - human
N;Alternate names: MAGE 3 protein
C;Spectes: Homo sapiens (man)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 18-Feb-2000
C;Accession: JC2361; PHI296; I38438
R;Ding, M.; Beck, R.J.; Keller, C.J.; Fenton, R.G.
Biochem. Biophys. Res. Commun. 202, 549-555, 1994
A;Title: Cloning and analysis of MAGE-1-related genes.
A;Reference number: JC2358; MUID:94311935
A;Accession: JC2361
                                                                       A:Molecule type: mRNA

A:Residues: 1-619 <VEI>

A:Cross references: EMBL:x80901; NID:g556677;

C:Superfamily: glucokinase regulator
                                                                                                                                                    glucokinase regulator - African clawed frog
c;Specles: Kenopus laevels (African clawed frog)
c;Specles: Kenopus laevels (African clawed frog)
c;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
c;Accession: S48729; S49339
c;Accession: S48729; S49339
c;Accession: S48729; S49339
c;Accession: S48729; MUID: Watelet, N.; van Schaftingen, E.
Eur. J. Biochem. 225, 43-51, 1994
A;Title: Cloning and expression of a Xenopus liver cDNA encoding a fructose.
A;Reference number: S48729; MUID: 95010134
A;Accession: S48729
A;Status: preliminary
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                           RESULT
S48729
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A; Residues: 1-314 < RES>
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A;Title: Human gene MAGE-3 codes for an antigen recognized on a melanoma by autologous A;Reference number: 138438; MUID:94157413
A;Accession: 138438
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A; Residues: 168-176 <TRA>
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A; Residues: 1-314 <DIN>
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Best Local
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Best Local Similarity
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Score 33;
Pred. No.
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    62
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                   Length 619;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-728 <SE3>
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A; Residues: 1-728 <MIY>
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A;Residues: 1-728 <WEI>
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A;Cross-references: GB:M29145; NID:g184041; PIDN:AAA52650.1; PID:g306846 R;Rubin, J.S.; Chan, A.M.L.; Bottaro, D.P.; Burgess, W.H.; Taylor, W.G.; Proc. Natl. Acad. Sci. U.S.A. 88, 415-419, 1991 A;Title: A broad-spectrum human lung fibroblast-derived mitogen is a vari A;Reference number: A39006; MUID:91110540 A;Accession: A39006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Experimental source: leukocyte
R;Miyazawa, K.; Tsubouchi, H.; Naka, D.; Takahashi, K.; Okigaki, M.; Arakaki, N.; Nak
Blochem. Blophys. Res. Commun. 163, 967-973, 1989
A;Title: Molecular cloning and sequence analysis of cDNA for human hepatocyte growth
A;Reference number: A33512; MOID:89392017
A;Accession: A33512
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R;Seki, T.; Ihara, I.; Sugimura, A.; Shimonishi, M.; Nishizawa, T.; Asami, O.; Hagiya Biochem. Biophys. Res. Commun. 321-327, 1990
A;Title: Isolation and expression of cDNA for different forms of hepatocyte growth fa A;Reference number: A36677; MUID:91025062
A;Accession: B36677;
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A; Title: Evidence for the identity of human scatter factor & A; Reference number: A41140; MUID:91334393
A; Accession: A41140
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C;Date: 17-Aug-1992 #sequence_revision 17-Aug-1992 #text_change 08-Dec-2000
C;Accession: JH0579; JU033; A41140; B36677; A36677; A33512; A39006; PH0114;
R;Seki, T.; Hagiya, M.; Shimonishi, M.; Nakamura, T.; Shimizu, S.
Gene 102, 213-219, 1991
R;Yoshiyama, Y.; Arakaki, N.; Naka, D.; Takahashi, K.; Hirono, Biochem. Biophys. Res. Commun. 175, 660-667, 1991 A;Title: Identification of the N-terminal residue of the heavy A;Reference number: PHO114; MUID:91207365
                                                                                                                               A;Molecule type: mRNA
A;Residues: 1-161,167-728 <RUB>
A;Cross-references: GB:M55379
A;Experimental source: embryonic lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-481, 'RT', 484-728 <SE2>
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A;Description: Organization of the human hepatocyte growth
A;Reference number: JU0333
A;Accession: JU0333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-728 <SEK>
A; Cross-references: DDBJ:D90318
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Cross-references: EMBL: X16323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-161,167-728 <SE4>
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S.
                                                                                                  S.; Kondo,
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                                                                                                  J.; Nakayam
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A; Accession: PHO
A; Molecule type:
A; Residues: 32-4
A; Experimental s
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A;Reference number: $06794; MUID:90066676
A;Accession: $06794
A;Accession: $06794
A;Molecula type: mRNA
A;Residues: 1-31, 'HK', 34-77,'N', 79-292,'Y', 294-299,'M', 301-316,'A', 318-335,'K', 337-386, A;Cross-references: EMBL:X16323; NID:932081; PIDN:CAA34387.1; PID:932082
A;Experimental source: liver
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R;Weidner, K.M.; Behrens, J.; Vandekerckhove, J.; Birchmeier, W.
J. Cell Blol. 111, 2097-2108, 1990
A;Fitle: Scatter factor: molecular characteristics and effect on the invasiveness of eparateric number: A37796; MUID:91035621
A;Reference number: A37796
A;Accession: A37796
A;Accession: A37796
A;Accession: A3796
A;Molecule type: protein
A;Residues: 86-91;329-344;356-363,'XX',366-370;425-434;442-447,'X',449-450;543-546,'X',A;Residues: 86-91;329-344;356-363,'XX',366-370;425-434;442-447,'X',449-450;543-546,'X',R;Residues: 86-91;329-344;356-363,'XX',366-370;455-434;442-447,'X',449-450;543-546,'X',R;Residues: 86-91;329-344;356-363,'XX',366-370;455-434;442-447,'X',449-450;543-447,'X',449-450;543-447,'X',449-450;543-447,'X',449-450;543-447,'X',449-450;543-447,'X',449-450;543-447,'X',449-447,'X',449-447,'X',449-447,'X',449-447,'X',449-447,'X',449-447,'X',449-447,'X',449-447,'X',449-447,'X',449-447,'X',449-447,'X',449-447,'X',449-447,'X',449-447,'X',449-447,'X',449-447,'X',449-447,'X',449-447,'X',449-447,'X',449-447,'X',449-447,'X',449-447,'X',449-447,'X',449-447,'X',449-447,'X',449-447,'X',449-447,'X',449-447,'X',449-447,'X',449-447,'X',449-447,'X',449-447,'X',449-447,'X',449-447,'X',449-447,'X',449-447,'X',449-447,'X',449-
A;Note: does not have proteinase activity
C;Superfamily: hepatocyte growth factor; kringle homology; trypsin homology
C;Roywords: alternative splicing; glycoprotein; growth factor; heterodimer; kringle; pyr
F;131/Domain: signal sequence #status predicted <SIG>
F;32-494,495-728/Product: hepatocyte growth factor #status experimental <MAT>
F;32-494/Domain: alpha chain #status experimental <ACH>
F;128-206/Domain: kringle homology <KR1>
F;211-288/Domain: kringle homology <KR3>
F;305-383/Domain: kringle homology <KR3>
F;391-469/Domain: kringle homology <KR4>
F;495-718/Domain: beta chain #status experimental <BCH>
F;495-716/Domain: trypsin homology <KR4>
F;394-402,566,653/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;487-604/Disulfide bonds: #status predicted
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A;Residues: 1-288,'ET' <HAR>
A;Residues: 1-288,'ET' <HAR>
A;Residues: 1-288,'ET' <HAR>
A;Cross-references: GB:L02931; NID:g184033; PIDN:AAA52649.1; PID:g184034
A;Cross-references: GB:L02931; NID:g184033; PIDN:AAA52649.1; PID:g184034
A;Miyazawa, K.; Kitamura, A.; Naka, D.; Kitamura, N.
Eur. J. Biochem. 197, 15-22, 1991
A;Title: An alternatively processed mRNA generated from human hepatocyte growth factor A;Reference number: $15443; MUID:91200041
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A;Note: part of this sequence, including the amino end of both the alpha and beta chains
R;Hartmann, G.; Naldini, L.; Weidner, K.M.; Sachs, M.; Vigna, E.; Comoglio, P.M.; Birchm
Proc. Natl. Acad. Sci. U.S.A. 89, 11574-11578, 1992
A;Title: A functional domain in the heavy chain of scatter factor/hepatocyte growth fact
A;Reference number: I59214; MUID:93087571
A;Accession: I59214
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A;Residues: 1-288, 'ET', 'MIY2>
A;Cross-references: EMBL:x57574; NID:g32083; PIDN:CAA40802.1; PID:g32084
A;Cross-references: EMBL:x57574; NID:g32083; PIDN:CAA40802.1; PID:g32084
R;Shima, N.; Nagao, M.; Ogakl, F.; Tsuda, E.; Murakami, A.; Higashio, K.
Blochem. Blophys. Res. Commun. 180, 1151-1158, 1991
A;Title: Tumor cytotoxic factor/hepatocyte growth factor from human fibroblasts: cloning A;Reference number: I52253; MUID:92062058
A;Reference number: I52253; MUID:92062058
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A;Cross-references: GDB:127524; OMIM:142409
A;Map position: 7q21.1-7q21.1
A;Introns: 30/1; 85/2; 123/1; 161/2; 209/1; 249/2; 289/1; C;Complex: disulfide-bonded heterodimer of chains derived C;Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Description: stimulates mitosis of hepatocytes and other cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GB:S62561; NID:g237996; PIDN:AAB20169.1; PID:g23799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 161-166 <SHI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Accession: S15443
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A; Note: does not have proteinase activity
C; Superfamily: hepatocyte growth factor; kringle homology trypsin homology
C; Keywords: alternative splicing; glycoprotein; growth factor; heterodimer; k
F; 1-32/Domain: signal sequence #status predicted <SIG>
F; 56-495/Product: hepatocyte growth factor #status predicted <MAT>
F; 56-495/Domain: kringle homology <KR1>
F; 129-207/Domain: kringle homology <KR2>
F; 121-289/Domain: kringle homology <KR3>
F; 302-470/Domain: kringle homology <KR3>
F; 392-470/Domain: kringle homology <KR3>
F; 392-470/Domain: kringle homology <KR3>
F; 496-728/Domain: kringle homology <KR3>
F; 496-728/Domain: kringle homology <KR4>
F; 496-728/Domain: kringle homology <KR4>
F; 496-719/Domain: kringle homology <KR4>
F; 496-719/Domain: trypsin homology <KR4-
F; 496-719/Domain: trypsin homology <KR4-
F; 496-719/Domain: trypsin homology <KR4-
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A;Residues: 1-728 <Table
A;References: GB:D90102; GB:M32987; NID:9220766; PIDN:BAA14133.1;
A;Rote: the authors translated the codon GAG for residue 70 as Gln, GAC
R;Okajima, A.; Miyazawa, K.; Kitamura, N.
Eur. J. Biochem. 193, 375-381, 1990
A;Title: Primary structure of rat hepatocyte growth factor and induction
A;Reference number: S13211; MUID:91031482
A;Accession: S13211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Tashiro, K.; Hagiya, M.; Nishizawa, T.; Seki, T.; Shimonishi, M.; Shimizu, S.; Naki
Proc. Natl. Acad. Sci. U.S.A. 87, 3200-3204, 1990
A;Title: Deduced primary structure of rath hepatocyte growth factor and expression of
A;Reference number: A35644; MUID:90222197
A;Accession: A35644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hepatocyte growth factor precursor - rat N;Alternate names: hepapoietin A; scatter factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F;33/Modified site: pyrrolidone carboxylic acid F;295,403,569,656/Binding site: carbohydrate (As F;488-607/Disulfide bonds: #status predicted
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A;Residues: 1-728 <OKA>
A;Cross-references: EMBL:X54400; NID:g56353; PIDN:CAA38266.1; PID:g4539554
C;Complex: disulfide-bonded heterodimer of chains derived from the same pr
hepatocyte growth factor precursor - mouse
N;Alternate names: hepapoietin A; Scatter factor
C;Species: Mus musculus (house mouse)
C;Date: 03-Mar-1993 #sequence_revision 26-May-1994 #text_change 16-Jun-2000
C;Accession: JC2117; PC2064; A60185; S43416; S45521; S17173; S10966; I48758;
R;Sasaki, M.; Nishio, M.; Sasaki, T.; Enami, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Description: stimulates mitosis of hepatocytes and other cells
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Date: 28-Sep-1990 #sequence_revision 18-Nov-1992 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A35644; S13211
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Pred. No.
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Pred. No.
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74;
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(Asn) (covalent) #status predicted
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A: Residues: 49-504 (SAA2)

Fromeson. E. H.; Marchewsky. 1.99

A: Title: purified softer factor stimulates epithelial and vascular endothelial cell mig

A: Reference number: 60185; MNID:90377927

A: Accession: A60185

A: Receidues: X', 184.186.0x; 191-192.7x', 194.7x', 197.357-364.7xx', 367;375-377.7E', 379.7

A: Residues: X', 184.186.0x; 191-192.7x', 194.7x', 197.357-364.7xx', 367;375-377.7E', 379.7

A: Relatives: X', 184.186.0x; 191-192.7x', 194.7xx', 197.357-364.7xx', 367;375-377.7E', 379.7

A: Relatives: X', 184.186.0x; 191-192.7x', 194.7xx', 197.357-364.7xx', 367;375-377.7E', 379.7

A: Relatives: X', 184.186.0x; 191-192.7x', 194.7xx', 197.357-364.7xx', 367;375-377.7E', 379.7

A: Relatives: X', 184.186.0x; 191-192.7x', 194.7xx', 197.357-364.7xx', 367;375-377.7E', 379.7

A: Relatives: X', 184.186.0x; 191-192.7x', 194.7xx', 197.357-364.7xx', 367;375-377.7E', 379.7

A: Relatives: X', 184.186.0x; 191-192.7x', 194.7xx', 197.357-364.7xx', 197.357-364.7xx
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A:Title: Identification of mouse mammary fibroblast-derived mammary growth factor as A:Reference number: JC2117; MUID:94183257
A:Accession: JC2117
A:Molecule type: mRNA
A:Residues: 1-728 <5852>
A:Cross-references: GB:D10212; NID:9220435; PIDN:BAA01064.1; PID:9220436
A:Experimental source: fibroblast, COS-1 cell
A:Note: submitted to JIPID, May 1993
A:Accession: PC2064
A:Molecule type: protein
A:Residues: 496-504 <582>
A:Residues: 496
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A. Molecule type: mRNA
A. Molecule type: mRNA
A. Residues: 1-415 <MATY
A. Gross-references: GB:L128010; NID:g452047; PIDN:AAC37584.1; PID:g452048
A. Gross-references: GB:L128010; NID:g452047; PIDN:AAC37584.1; PID:g452048
A. Gross-references: GB:L128010; NID:g452047; PIDN:AAC37584.1; PID:g452048
A. Molecule tis uncertain whether Met-1 or Met-2 is the initiator
R. McDonald, H.; Smailus, D.; Jenkins, H.; Adams, K.; Simpson, N.E.; Good:
Genomics 13, 344-348, 1992
A. Fitle: Identification and characterization of a gene at D10S94 in the language of the property of the language of the langu
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R;Matunis, M.J.; Xing, J.; Dreyfuss, G.
Nucleic Acids Res. 22, 1059-1067, 1994
A;Title: The hnRNP F protein: unique primary structure, A;Reference number: S43484; MUID:94203790
A;Accession: S43484
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C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999
C;Date: 12-Jun-1999 #sequence_revision 11-Jun-1999
C;Accession: E72352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F:496-728/Domain: hepatocyte growth factor beta chain *status F:496-719/Domain: trypsin homology <TRY>
F:33/Modified site: pyrrolidone carboxylic acid (Gln) (in matu F:295,403,559,655/Binding site: carbohydrate (Asn) (covalent) F:488-607/Disulfide bonds: *status predicted
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C;Species: Homo sapiens (man)
C;Date: 27-Jan-1995 #sequence_revision
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C; Superfamily:
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A; Experimental source: strain
C; Genetics:
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A; Molecule type: mRNA
A; Regidues: 2-415 < MC
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A; Title: Ev
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A; Residues: 1-350 < ARN>
                                                             A; Status: not compared with conceptual translation
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2; Mismatches
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; Phillips, C.A.; Richardson,
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A;Cross-reterences: ob. A. C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A;Experimental source: strain 9a5c
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Carraro, D.M.; Carrer, H
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H
as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.;
submitted to GenBank, June 2000
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigu
Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E
A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
F.G.; Nupes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.F
Rodriques, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
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J. Biol. Chem. 270, 28780-28789, 1995
A;Title: Heterogeneous nuclear ribonuclearproteins H, H', and F are members of a ubiquit A;Reference number: A57806; MUID:96081943
A;Reference number: A57806; MUID:96081943
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-449 < RES>
A;Residues: 1-449 < RES>
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A;Gene: GDB:HNRPF
A;Cross-references: GDB:5429144; OMIM:601037
A;Map position: 10q11.21-10q11.22
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C;Species: Xylella fastidiosa
C;Species: Alg-2000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000
C;Accession: E82849
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen Nature 406, 151-157, 2000
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A;Cross-references: GDB:5428597;
A;Map position: 5q35.3-5q35.3
                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Title: The genome sequence of the plant pathogen Xylella fastidiosa. A; Reference number: A82515; MUID:20365717
A; Note: for a complete list of authors see reference number A59328 below
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A; Residues: 1-101 <SIM>
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A; Status: preliminary
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85.7%;
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85.7%;
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Pred. No. 70;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GDB:626033; OMIM:601035
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Pred. No.
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64;
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A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silva, M.A.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L. A;Reference number: A59328
A;Contents: annotation
C;Genetics:
A;Gene: XF0095
C;Superfamily: Mcthanococcus jannaschii conserved hypothetical protein MJ0652
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Qy
В
                                Matches
                                       Query Match
Best Local
79
               1 RIGHLYIL 8
RIGHIAIL 86
                                Similarity 6; Conserv
                                Conservative
                                         73.8%;
75.0%;
                                 1;
                                         Score 31; DB Pred. No. 21;
                                   Mismatches
                                                  2;
                                                  Length 101;
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0;

Search completed: June 20, 2001, 14:04:35 Job time: 82 sec

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Minimum DB
Maximum DB
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Perfect score:
Sequence:
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Maximum Match 100%
Listing first 45 s
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        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq
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    protein search, using sw model
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Match
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Copyright (c) 1993 - 2000 Comp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RIGHLYIL 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
    DB
  MAGC_HUMAN
GCKR_XENLA
HGF_HUMAN
HGF_MOUSE
HGF_RAT
ROF_HUMAN
ROH1_HUMAN
ROH1_HUMAN
ROH2_HUMAN
GYRB_BARBA
TIFA_PACYU
Y077_HAEIN
PQQB_ACICA
MAGG_HUMAN
TGT_ARCFU
CDS1_SOYBN
CS3_SOYBN
CS3_SOYBN
CS3_SOYBN
CS3_SOYBN
CFGL_BPK11
POLG_BPK11
POLG_BPK11
POLG_BPUDN
RPON_ARCFU
RPON_BCSU
RPON_ARCFU
RPON_BCSU
RPON_ARCFU
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P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Description
homo sapien
homo sapien
record a construction
mus musculu
rattus nory
homo sapien
hartonella
phartonella
phareophilus
acinetobact
homo sapien
homo sapien
homo sapien
archaeoglob
a phosphati
homo sapien
                                           InterPro: IPR002190: -.
Pfam: PF01454; MAGE; 1.
Antigen; Multigene family
DOMAIN 40 43
CONFLICT 10 10
CONFLICT 187 187
CONFLICT 300 300
SEQUENCE 314 AA; 34802
                                                                                                                                                                                           EMBL; L18877; AAA19023.1; MIM; 300177; -.
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| 45 | 44 | 43 | 42 | 41 | 40 | 39 | 38 | 37 | 36 | 35 | 34 |
|--------------------|--------------------|------------|--------------------|------------|------------|----------|------------|------------|--------------------|-----------|--------------------|
| 29 | 29 | 29 | 29 | 29 | 29 | 29 | 29 | 29 | 29 | 29 | 29 |
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| XP55_STRLI | DNB2_ADE04 | YG08_SYNY3 | SGAA_HYPME | GCST_HUMAN | GCST_BOVIN | KCC1_RAT | KCC1_HUMAN | SNC1_HUMAN | FLIM_AGRTU | EXO5_BPT5 | AMOA_NITEU |
| P06109 streptomyce | P06500 human adeno | | 008374 hyphomicrob | | | | | | Q44457 agrobacteri | | Q04507 nitrosomona |

ALIGNMENTS

| 888888888 | \$ | RRC RRL | REST MAGG ID AC DT DT DT DT DT DT OS OC |
|--|--|---------|--|
| This SWISS-PROT between the Swi the European Bio use by non-pro modified and thi entities require or send an email | | | RESULT 1 MAGC_HUMAN STANDARD; PRT; 314 AA. ID MAGC_HUMAN STANDARD; PRT; 314 AA. AC P43565; DT 01-NOV-1995 (Rel. 32, Created) DT 01-NOV-1995 (Rel. 32, Last sequence update) DT 15-JUL-1999 (Rel. 38, Last annotation update) DE MELANOMA-ASSOCIATED ANTIGEN 12 (MAGE-12 ANTIGEN) (MAGE12D) GN MAGEAL2 OR MAGE12. OS HOMO sapiens (Human). OC ENKaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. OK MAGMAIA; Eutheria; Primates; Catarrhini; Hominidae; Homo. |
| on ts ay al | : | | |

'; Tumor antigen.

POLY-SER.

C -> S (IN REF. 2).

A -> D (IN REF. 2).

P -> S (IN REF. 2).

N#; 3F0787CECD8816A5 C.

MW;

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                                                                                          Query Match
Best Local
                                                            Matches,
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P43357;
01-NOV-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     between the Swiss Institute of Bloinformatics the European Bloinformatics Institute. There as use by non-profit institutions as long as immodified and this statement is not removed. Use entities requires a license agreement (See http or send an email to license@isb-sib.ch).
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between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ding M., Beck R.J., Keller C.J., Fenton R.G.;

"Cloning and analysis of MAGE-1-related genes.";

"Cloning and analysis of MAGE-1-related genes.";

Biochem. Blophys. Res. Commun. 202:549-555(1994).

-I- FUNCTION: NOT KNOWN, THOUGH MAY PLAY A ROLE IN EMBRYONAL

DEVELOPMENT AND TUMOR TRANSFORMATION OR ASPECTS OF TUMOR

PROGRESSION. ANTIGEN RECOGNIZED ON A MELANOMA BY AUTOLOGOUS

CYTOLYTIC T LYMPHOCYTES.

-I- TISSUE SPECIFICITY: EXPRESSED IN MANY TUMORS OF SEVERAL TYPE

-I- TISSUE SPECIFICATIVE EXPRESSED IN MANY TUMORS OF SEVERAL TYPE

-I- TISSUE SPECIFICATIVE EXPRESSED IN MANY TUMORS OF SEVERAL TYPE

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-I- TISSUE SPECIFICATIVE SPECI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaugler B., van den Eynde B., van der Bruggen P., F
Gaforio J.J., de Plaen E., Lethe B., Brasseur F., E
"Human gene MAGE-3 codes for an antigen recognized
autologous cytolytic T lymphocytes.";
J. Exp. Med. 179:921-930(1994).
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01-NOV-1995 (Rel. 32, Last sequence update)
15-70L-1999 (Rel. 38, Last annotation update)
MELANOMA-ASSOCIATED ANTIGEN 3 (MAGE-3 ANTIGEN) (ANTIGEN MZ2-D).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human
Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MAGEA3 OR MAGE3
                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U03735; AAA17446.1;
MIM; 300174; -.
                                                                                                                                                                                                                                                                                       MUTAGEN
                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF01454; MAGE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR002190; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-94311935; PubMed=8037761;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-Skin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=94157413; PubMed=8113684;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
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      2 IGHLYI 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE SPECIFICITY: EXPRESSED IN MANY TUMORS OF SEVERAL TYPES, SUCH AS MELANOMA, HEAD AND NECK SQUAMOUS CELL CARCINOMA, LUNG CARCINOMA AND BREAST CARCINOMA, BUT NOT IN NORWAL TISSUES EXCEPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: BELONGS TO THE MAGE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FOR TESTES AND PLACENTA. NEVER EXPRESSED LEUKEMIAS AND LYMPHOMAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SWISS-PROT entry is copyright. It is produced through a collaboration -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
8; Conserv
                                                               Similarity 6; Conserv
                                                                                                                                                                                                                                                     Multigene family; Tumor antigen.
40 43 POLY-SER.
170 170 D->A; ABOLISE
176 176 Y->A; ABOLISE
                                                                                                                                                                                                                          314 AA;
                                                               78.6%; Silarity 100.0%; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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tazoa; Chordata;
heria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                            43
170
176
34747 )
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                                                                                                                                                                                                                             MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   . '
                                                               Score 33; DB; Pred. No. 14; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                          D->A: ABOLISHES HLA-A1 BINDING. Y->A: ABOLISHES HLA-A1 BINDING; 3F5EB13D1C9946A1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 42; DB 1;
Pred. No. 0.21;
Mismatches (
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Catarrhini;
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he B., Brasseur F., Boon T.,
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SEQUENCE
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InterPro; IPR001741;
Pfam; PF01380; SIS; 1
                                                                                                                                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
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HGF OR HPTA.
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use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by entities requires a license agreement '...
SEQUENCE FROM N.A.

MEDLINE=91340155; PubMed=1831432;
Seki T., Hagiya M., Shimonishi M., Nakamura T.,

Sorganization of the human hepatocyte growth faw
                                                                                                                                                                                                              HGF_HUMAN STANDARD; PRT; 728 AA P14210; P14210; O1-JAN-1990 (Rel. 13, Created) O1-AUG-1991 (Rel. 19, Last sequence update) O1-OCT-2000 (Rel. 40, Last annotation update) HEPATOCYTE GROWTH FACTOR PRECURSOR (SCATTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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PS01272; GCKR; 1.
619 AA; 68738
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Primates;
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license agreement (See http://www.isb-sib.ch/announce/
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Pred. No.
                                                                                                                    Craniata; Vertebrata;
Catarrhini; Hominidae
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Pred. No. 29;
Mismatches
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(SCATTER F
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    factor encoding gene.";
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                        Shimizu
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Gene

102:213-219(1991).

SEQUENCE FROM N.A.

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TISSUB-Leukocyte;
RISSUB-Leukocyte;
RISSUB-Leukocyte;
RISSUB-Leukocyte;
REDLINE-91025062; PubMed-2145836;
MEDLINE-91025062; PubMed-2145836;
Seki T., Ihara I., Sugimura A., Shimoishi M., Nishizawa Asami O., Hagiya M., Nakamura T., Shimizu S.;
Rami O., Hagiya M., Nakamura T., Shimizu S.;
Risolation and expression of cDNA for different forms of growth factor from human leukocyte.";
qrowth factor from human leukocyte.";
Structure [10]
                                                                                                                                                                    MEDLINE-92331602; PubMed-1321034;
Lokker N.A., Mark M.R., Luis E.A., Bennett G.L., Robbins |
Baker J.B., Godowski P.J.;
"Structure-function analysis of hepatocyte growth factor:
identification of variants that lack mitogenic activity ye
high affinity receptor binding.";
EMBO J. 11:2503-2510(1992).
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MEDLINE-91334393; PubMed-1831266;
Weidner K.M., Arakaki N., Hartmann G.,
Rieder H., Fonatsch C., Tsubouchi H.,
                                                                                                                                                                                                                                                                                                                                                                       "Hepatocyte growth factor is linked on the alpha chain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nakamura T., Nishizawa T., Hagiya
Sugimura A., Tashiro K., Shimizu S
"Molecular cloning and expression
Nature 342:440-443(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Molecular cloning and growth factor."; Biochem. Biophys. Res.
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Proc. Natl. Acad.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CARBOHYDRATE-LINKAGE SITE 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Identification of the N-terminal residue of the heavy on native and recombinant human hepatocyte growth factor.", Biochem. Biophys. Res. Commun. 175:660-667(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hishida T., Daikuhara Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nakayama H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Birchmeier W.; "Evidence for the
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                                      Rubin J.S., Bottaro D.P., F
"The solution structure of
factor reveals a potential
                                                                                                           STRUCTURE BY NMR OF MEDLINE-98154323; Pu
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                                                                                           Mazzulla
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                                                                                                                                                                                                                                                                                                                                                    Biophys.
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H., Gohda E., Kitamura
                    veals a potential heparin-binding
6:109-116(1998).
                                                                         54323; PubMed=9493272;
zzulla M.J., Kaufman J.D.,
Bottaro D.P., Byrd R.A.;
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Hirono S.,
                                                        Byrd R.A.;
f the N-terminal domain
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of human hepatocyte growth factor.";
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Hishida T., Daik
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           factor at 2.0-A resolution.";
Structure 6:1383-1393(1998).
-!- FUNCTION: HGF IS A POTENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ultsch M., Lokker N.A., Godowski P.J., "Crystal structure of the NK1 fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) MEDLINE=99036858; PubMed=9817840;
                                                                                                                                                                                                                                                                                                                                                             SUBUNIT: DIMER OF DISULFIDE BOND.
                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION: HGF IS A POTENT MITOGEN FOR MATURE PARENCHYMAL HEPATOCYTE CELLS, SEEMS TO BE AN HEPATOTROPHIC FACTOR, AND AS GROWTH FACTOR FOR A HEPAD SPECTRUM OF TISSUES AND CELL IT HAS NO DETECTABLE PROTEASE ACTIVITY.
                                                                                                                                                                              s SWISS-PROT entry is copyright. It is produced ween the Swiss Institute of Bioinformatics and European Bioinformatics Institute. There are r
                                                                                                                                                                                                                                                                                                            SIMILARITY: CONTAINS 4 KRINGLE REGIONS. SIMILARITY: BELONGS TO PEPTIDASE FAMILY
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BAA14348.1;
BAA14348.1;
                                                                                                                                                                                                                                                                                                                                                                                       AN ALPHA CHAIN AND A BETA CHAIN LINKED
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of human hepatocyte growth
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Pram; Process, Aringle; 4.

Pfam; PF00089; trypsin; 1.

PRINTS; PR00018; KRINGLE.

PRINTS; PR00722; CHYMOTRYPSIN.

PROSITE; PS00021; KRINGLE_1; 4.

PROSITE; PS50070; KRINGLE_2; 4.

PROSITE; PS50070; KRINGLE_2; 5.
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L; D90329; BAA14348.1; JC
L; D90330; BAA14348.1; JC
L; D90331; BAA14348.1; JC
L; D90332; BAA14348.1; JC
L; D90333; BAA14348.1; JC
L; D90333; BAA14348.1; JC
L; M29145; AAA52650.1; JC
L; M60718; AAA5264.1; JC
L; M60718; AAA5264.1; JC
L; M6323; CAA34387.1; JC
M73239; AAA64239.1; JC
M73240; AAA64297.1; JC
M73240; AAA64239.1; JC
M73240; AAA64280; 
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D90323;
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D90318;
D90319;
D90320;
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                                                                                                                                                                                                                                                                                                                                                                                                            3D-structure
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RESULT
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Best Local
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                                          TISSUE-Liver;
TISSUE-Liver;
MEDLINE-94363381; PubMed-8081873;
Lee C.C., Kozak C.A., Yamada K.M.;
""""""""" genetic mapping, and expression
                                                                                                                                                                                                 Q08048: Q64007; Q61662;
01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
HEPATOCYTE GROWTH FACTOR PRECURSOR (SCATTER FACTOR) (SF)
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CARBOHYD
CARBOHYD
 TISGUENCE FROM N.A.
TISSUE-Liver;
MEDILINE-94060105; PubMed-8241272;
Liu Y., Michalopoulos G.K., Zarne
                                                                                                             MEDLINE=94183257; PubMed=8135822;
Sasaki M., Nishio M., Sasaki T., Enami J.;
"Identification of mouse mammary fibroblast-derived
                                                                                                                                                               Mus musculus (Mouse)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                         TISSUE=Mammary fib
MEDLINE=94183257;
                                                                                                                                   SEQUENCE FROM N.A., AND SE
TISSUE=Mammary fibroblast;
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                                                                                                      factor as hepatocyte growth factor.
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630 RVAHLYIM
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5; Conserv
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                                     Commun.
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83133
                                                                                                                                                                Chordata;
Rodentia;
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                                                                                                                                                                                                                                                                                                                78.6%;
62.5%;
                                                                                               Commun. 199:772-779(1994).
                                                                                                                                          SEQUENCE
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 Zarnegar
                                                                                                                                                                                                                                                                                                                                                     SCD CHD HE CLX X OR
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N-LINKED
QR -> HK
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N-LINKED (GLCNAC. . .) (PO
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SERINE PROTEASE-LIKE.
                                                                                                                                                           Craniata; Vertebrata; Euteleosic
Sciurognathi; Muridae; Murinae;
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V A (IN REF. 4)
V K (IN REF. 4)
V N (IN REF. 4)
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V I (IN REF. 4)
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                                                                                                                                          OF.
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(GLCNAC...)
(IN REF. 4).
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Query Match Best Local S Matches

Similarity 5; Conser

Conservative

2;

1;

Indels

0,:

Gaps

0;

78.6%;

Score 33; DB Pred. No. 34; 2; Mismatches

1;

Length 728,

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MGD; MGI:96079; Hgf.
Interpro; IPR000001; -.
Interpro; IPR001254; -.
Interpro; IPR001314; -.
Interpro; IPR003014; -.
                                                                                                                                                                                                                                                                               Pfam; PF00024; PAN; 1.
Pfam; PF00051; kringle; 4.
Pfam; PF00089; trypsin; 1.
Pfinn; PF00089; trypsin; 1.
PRINTS; PR00018; KRINGLE.
PRINTS; PR00722; CHYMOTRYPSIN.
PROSITE; PS00021; KRINGLE_1; 4.
PROSITE; PS00021; KRINGLE_2; 4.
Growth factor; Kringle; Glycoprotein; Serine protease homolog;
  CARBOHYD
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entitles requires a license agreement (See l
or send an email to license@isb-sib.ch).
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-i- EUNCTION: HGF IS A POTENT MITOGEN FOR MATURE PARENCHYMAL HEPATOCYTE CELLS, SEEMS TO BE AN HEPATOCYTE CELLS. SEEMS TO BE AN HEPATOCYTE AND CELL TI HAS NO DETECTABLE PROTEASE ACTIVITY.
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SUBUNIT: DIMER OF AN ALPHA CHAIN AND A
DISULFIDE BOND.
ALTERNATIVE PRODUCTS: A SHORT FORM OF I
ALTERNATIVE RNA SPLICING. THE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY:
SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRYPSIN FAMILY. PLASMINOGEN SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                              ; D10212; BAA01064.1;
, D10213; BAA01065.1;
,; S71816; AAB31855.1;
,; X72307; CAA51054.1; /
; P14210; 2HGF.
                                                                                                                                                                                                                                                                            Alternative
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129
212
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N -> K (IN REF. 2).

V -> L (IN REF. 2).

R -> H (IN REF. 3).
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KRINGLE
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KRINGLE
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BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                             HEPATOCYTE GROWTH FACTOR ALPHA CHAIN HEPATOCYTE GROWTH FACTOR BETA CHAIN. PYRROLIDONE CARBOXYLIC ACID
                                                                                                                                                                                                                   (BY
                                                                                                                                                                                                                                                                  BY SIMILARITY
 -> L (IN REF. 2)
-> H (IN REF. 3)
A0381FC497534328
                                                                                                                                                                                                                    SIMILARITY).
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A OKajina A., Miyazawa K., Kitamura N.;

Primary structure of rat hepatocyte growth factor and induction of the sum of the su
                                                                                                     Pfam; PF00024; PAN; 1.
Pfam; PF00025; kringle; 4.
Pfam; PF000089; trrpgsin; 1.
PRINTS; PR00018; KRINGLE.
PRINTS; PR00722; CHYMOTRYPSIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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between
                                         PROSITE; PS00021; KRINGLE_1; 4.
PROSITE; PS50070; KRINGLE_2; 4.
Growth factor; Kringle; Glycopr
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PIR; S
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InterPro; IPR001254; -.
InterPro; IPR001314; -.
InterPro; IPR003014; -.
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                                                                                                                                                                                                                                                                                                                MEROPS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Mammalia; Eutheria; NCBI_TaxID=10116;
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P17945;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Toshiro K., Hagiya M., Nishizawa T.,
Shimizu S., Nakamura T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-WISTAR;
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01-NOV-1990 (Rel. 16, Last sequence
15-JUL-1998 (Rel. 36, Last annotati
HEPATOCYTE GROWTH FACTOR PRECURSOR
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MEDLINE=90222197; PubMed=2139229;
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S13211; S13211.
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A HONORE B., RASMUSSEN H.H., VORUM H., Dejgaard K., Liu X.,
A HONORE B., RASMUSSEN H.H., VORUM H., Dejgaard K., Liu X.,
A Gromov P., Madsen P., Gesser B., Tommerup N., Celis J.E.;
THE TAMEST AND THE TEROGENOUS THE STROTEIN (HNRN) COMPLEXES WHICH PROVIDE THE SUBSTOR THE PROCESSING EVENTS THAT PRE-MRNAS UNDERGO BEFORE BEFORE BEFORE THE PROCESSING EVENTS THAT PRE-MRNAS IN THE CYTOPLASM. PROBABLY CONTINUAR, LOCATION: RICHEAR; NUCLEOPLASM.

C -!- SUBCELLULAR LOCATION: EXPRESSED UBIQUITOUSLY.
-!- SIMILARITY: CONTAINS 3 RNA RECOGNITION MOTIFS (RRM).
-!- SIMILARITY: CONTAINS 3 RNA RECOGNITION MOTIFS (RRM).
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ROF_HUMAN
P52597;
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on at use by non-profit institutions as long as its content is in no was modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce
                                                                                                                                                                                                                                                                                                        MEDINE-94203790; pubMed-7512260; MEDINE-94203790; pubMed-7512260; Matunis M.J., Xing J., Dreyfuss G.; "The hnRNP F protein: unique primary structure, properties, and subcellular localization."; Nucleic Acids Res. 22:1059-1067(1994).
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Mammalia; Eutheria;
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US NUCLEAR RIBONUCLEOPROTEIN F (HN
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Chordata;
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SERINE PROTEASE-LIKE.
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01-OCT-1996
01-OCT-2000
                                    PIOTEIN dATABASE OF NORMAI human epidermal keratinocytes.";
Electrophoresis 13:960-969(1992).

-I- FUNCTION: THIS PROTEIN IS A COMPONENT OF THE HETEROGENOUS NUCLEA RIBONUCLEOPROTEIN (HNRNP) COMPLEXES WHICH PROVIDE THE SUBSTRATE FOR THE PROCESSING EVENTS THAT PRE-MRNAS UNDERGO BEFORE BECOMING FUNCTIONAL, TRANSLATABLE MRNAS IN THE CYTOPLASM. BINDS POLY (RG)
-i- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOPLASM.
-i- TISSUE SPECIFICITY: EXPRESSED UBIQUITOUSLY.
-i- DOMAIN: EACH QUASI-RRM REPEAT BOUND POLY (RG), WHILE ONLY THE N-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Honore B., Rasmussen H.H., Vorum H., Dejgaard K., Liu X., Gromov P., Madsen P., Gesser B., Tommerup N., Celis J.E.; "Heterogeneous nuclear ribonucleoproteins H. H', and F are a ubiquitously expressed subfamily of related but distinct encoded by genes mapping to different chromosomes."; J. Biol. Chem. 270:28780-28789(1995).
                                                                                                                                                                                                                                         Rasmussen H.H., van Damme J., Puype M., Gess
Vandekerckhove J.;
"Microsequences of 145 proteins recorded in
                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=94203790; PubMed=7512260; Matunis M.J., Xing J., Dreyfuss G.; "The hnRNP F protein: unique primary structure, properties, and subcellular localization."; Nucleic Acids Res. 22:1059-1067(1994).
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Eukaryota; Metazoa;
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01-OCT-1996 (Rel. 34,
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HETEROGENEOUS NUCLEAR
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Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 D14E170631FB1F31 CRC64
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                      POLY (RU).
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31;
                                                                                                                                                                                                                                                                                      Gesser B.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     H (HNRNP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           nucleic acid-binding
                           NONE
                                                                                                                                                                                                                                             two-dimensional
                                                                                                                                                                              HETEROGENOUS NUCLEAR
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RESULT 9
ROH2_HUMAN
    ATORRA RAPPRARA
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between
the Euro
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or send a
                                                                  SEQUENCE
Oeltjen J
Belmont J
                                                                                                     "Isolation of cosmid and cl
BTK gene at Xq21.3-q22.";
Genomics 21:517-524(1994).
                                                                                                                                                                                                                           01-NOV-1997 (Rel. 35,
01-NOV-1997 (Rel. 35,
01-OCT-2000 (Rel. 40,
HETEROGENEOUS NUCLEAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
DOMAIN
          PARTIAL SEQUENCE FROM N.A.
MEDLINE=96081943; PubMed=7499401;
HONOTE B., Rasmussen H.H., Vorum H., Dejgaard K.,
Gromov P., Madsen P., Gesser B., Tommerup N., Cel.
                                                                                                                                   Zhou
                                                                                                                                          MEDLINE=95048329; PubMed=7959728; Vorechovsky I., Vetrie D., Hollan
                                                                                                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                       P55795;
01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS50102; RRM; 3. PROSITE; PS00030; RRM_RNP_1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Aarhus/Ghent-2DPAGE;
Aarhus/Ghent-2DPAGE;
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                                                         Submitted
                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                           Homo
                                                                                                                                                                                                                     HNRPH2 OR FTP3
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                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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                                                                                                                                                                                                                                                                                                                       175 RIGHRYI 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     s SWISS-PROT entry is copyright. It is produced ween the Swiss Institute of Bioinformatics and European Bioinformatics Institute. There are
                                                                                                                                                                                                                                                                                                                                | RIGHLYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: CONTAINS 3 RNA RECOGNITION MOTIFS (RRM).
                                                                                                                                 chovsky I., Vetrie D., Holland J., J.N., Notarangelo L.D., Plebani A
                                                                                                                                                                                                           sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            601035;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 L22009; AAA91346.1;
                                                                    4
                                                                                                                                                                                                                                                                                                                                                         Similarity 85.7 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           non-profit institutions as long as its content is and this statement is not removed. Usage by and for requires a license agreement (See http://www.isb-sib-
                                                                   FROM
                                                                                                                                                             FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IPR000504;
                                                          (NOV-1996)
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                                                                                                                                                                                          (Human).

'aroa; Chordata;

'artes;
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, Liu X.,
, Gibbs R
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    nuclear
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372
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4429;
5416;
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85
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Last annotation update)
RIBONUCLEOPROTEIN H' (HNRNP
                                                                   A.
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                                                                                                                                                                                                                                                        Created)
    ribonucleoproteins
                                                         the
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                                                                                                                          cDNA clones
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RNA-BINDING (RRM) 2.
RNA-BINDING (RRM) 3.
2 X 16 AA GLY-RICH P
                                                                                                                                                                                                                                                                                                                                                                  Score 32;
Pred. No.
                                                          EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FALSE_NEG.
Ribonucleoprotein;
                                                                            Malley
                                                                                                                                                                                                  Craniata; Vertebrata;
                                                                                                                                                                                                                                                                           PRT;
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                                                                            T.M.,
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    Η.,
                                                                            Allen
., Celis J.E.;
N., Celis J.E.;
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                                                                                                                         region
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                                                                           R.C.,
                                                                                                                                                                                                                                                                                                                                                                                                       CRC64;
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L outstation -
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RESULT 10
C312_DROME
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Best Local
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J. Biol. Chem. 270:28780-28789(1955).

-I. FUNCTION: THIS PROTEIN IS A COMPONENT OF THE HETEROGENOUS NUCLEAR RIBONUCLEOPROTEIN (HNRNP) COMPLEXES WHICH PROVIDE THE SUBSTRATE FOR THE PROCESSING EVENTS THAT PRE-MRNAS UNDERGO BEFORE BECOMING FUNCTIONAL, TRANSLATABLE MRNAS IN THE CYTOPLASM. BINDS POLY (RG).

-I. SUBCELLULLAR LOCATION: NUCLEAR; NUCLEOPLASM.
-I. TISSUE SPECIFICITY: EXPRESSED UBIQUITOUSLY.
-I. SIMILARITY: CONTAINS 3 RNA RECOGNITION MOTIFS (RRM).
SEQUENCE FROM N.A.

STRAIN-BERKELEY;

MEDLINE-20196006; PubMed=10731132;

MEDLINE-20196006; PubMed=10731132;

Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfelifer B.D.,

Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G
                                                                                                                                                                                                                                                                                                                      C312_DROME STANDARD; PRT; 510 AA.

GYVVN5;
01-OCT-2000 (Rel. 40, Created)
01-OCT-2000 (Rel. 40, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
PROBABLE CYPOCHROME P450 312A1 (EC 1.14.-.)

CYP312A1 OR CG5137.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REPEAT
SEQUENCE
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REPEAT
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long as its content is inconfined and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Arthropoda; Trac
Pterygota; Neoptera; Endopterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
DOMAIN
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                                                                                                                                                                                                                                       Ephydroidea;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U01923; -; NOT_ANNOTATED_CDS EMBL; U78027; AAB64202.1; -.
                                                                                                                                                                                                                                                                                                    Drosophila melanogaster (Fruit fly).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the Ewent and the Experimental Swiss Institute. There are no restropy by non-profit institutions as long as its content
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        601036;
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                                                                                                                                                                                                                                       Drosophilidae;
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85.7%;
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Drosophila.
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RNA-BINDING (RRM) 1.
RNA-BINDING (RRM) 2.
RNA-BINDING (RRM) 3.
2 X 16 AA GLY-RICH AF
1-1.
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                                                                                                                                                                                                                                                                                 Tracheata;
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    Nelson C.R., Miklos G.L.G.
                                                                                                                                                                                                                                                        Hexapoda; Insecta; a; Brachycera; Musc
                                                                                                                                                                                                                                                                                                                                          (CYPCCCXIIA1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 449
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MAG2_HUMAN ID MAG2_H AC P43356

MAG2_HUMAN P43356;

STANDARD;

PRT;

314

RESULT 11

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                                                                                                                                                                                              RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Ra Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Ra Belson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Ra Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., Rottier R., Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davles P., Ra Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davles P., Ra Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davles P., Ra Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davles P., Ra Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davles P., Ra Cherry J.M., Davis R., Dunkov B.C., Dunn P., Ra Cherry J.M., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W., Ra Cherry C., Gabriellan A.E., Garg N.S., Gelbart W.M., Glasser K., Ra Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibeywam C., Ra Glodek A., Gong F., Gorrell J.H., Gu Z., Kennison J.A., Ketchum K.A., Alasin F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Alasin F., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Lia Z., Liang Y., Lin X., Ra Lasko P., Lei Y., Levitaka A.A., Li J., Li Z., Liang Y., Lin X., Ra Lasko P., Lei Y., Levitaka A.A., Li J., Li Z., Liang Y., Lin X., Ra Merkulov G., Milshina N.V., McLeod M.P., McPherson D.L., Ra Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Ra Merkulov G., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Ra Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Ra Ra Harris S.M., Woodage T., Worley B., Wang A.H., Wang X., Ra Weight B.C., Scheeler F., Shen H., Shen H., Shen B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Ra Ra Keinert K., Ra Ming J.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Ra Zheng X.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Ra Zheng X.-H., Wang S., Yao Q.A., Yeh R.-F., Zaveri J.S., Shan M., Zhang G., Zhao Q.A., Smith H.O., Ra Zheng X.-H., Keng S., Yao Q.A., Shan M., Weissenbach J., Smith H.O.,
                                                                                   Matches
                                                                                                         Query Match
Best Local
                                                                                                                                                                                     PROSITE; PS00086; CYTOCHROME_P450; FALSE_NEG.
Oxidoreductase; Monooxygenase; Membrane; Heme; Microsome;
Endoplasmic reticulum; Hypothetical protein.
BINDING 455
HEME (BY SIMILARITY).
SEQUENCE 510 AA; 58804 MW; 6973570BF911E4E0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         between the Swiss Institute of Bioinformat
the European Bioinformatics Institute. The
use by non-profit institutions as long
modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -i- FUNCTION: MAY BE INVOLVED IN THE METABOLISM OF INSECT HORMONES
IN THE BREAKDOWN OF SYNTHETIC INSECTICIDES (BY SIMILARITY).
-i- CATALYTIC ACTULTY: H+ REDUCED FLAVOPROTEIN + O(2) = ROH +
OXIDIZED FLAVOPROTEIN + H(2)O.

-i- SUBCELLULAR LOCATION: MEMBRANE-BOUND. ENDOPLASMIC RETICULUM
                                                                                                                                                                                                                                                                               PRINTS; PR00385; P450.
PROSITE; PS00086; CYTO
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43
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                                          2 IGHLYIL
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IGHLHIL
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                                             MURC_BUCAI STANDARD; PRT; 484 AA. P57310; 01-OCT-2000 (Rel. 40, Created) 01-OCT-2000 (Rel. 40, Last sequence update) 01-OCT-2000 (Rel. 40, Last annotation update) UDP-N_ACETYLMURAMATE--ALANINE LIGASE (EC 6.3.2.8)
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SEQUENCE
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J. Exp. Med. 179:921-930(1994).

-i- FUNCTION: NOT KNOWN, THOUGH MAY PLAY A ROLE IN EMBRYONAL
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MEDLINE=94102805; PubMed=8276455;
de Smet C., Lurquin C., van der E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
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01-NOV-1995 (Rel. 32, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation updat
ACETYLMURAMOYL-L-ALANINE MURC OR BU215.
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InterPro; IPR002190; -.
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MELANOMA-ASSOCIATED ANTIGEN 2 (MAGE-2 ANTIGEN).
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PROGRESSION. ANTIGEN RECOVER.

CYTOLYTIC T LYMPHOCYTES.

CYTOLYTIC T LYMPHOCYTES.

TISSUE SPECIFICITY: EXPRESSED IN MANY TUMORS OF SEVERAL 11

TISSUE SPECIFICITY: EXPRESSED IN MANY TUMORS OF SEVERAL 11

TISSUES TO ARCTNOMA, BUT NOT IN NORMAL TISSUES
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Primates;
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85.7%;
                             SYNTHETASE)
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POLY-SER.
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Catarrhini; Hominidae; Homo
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Q59189;
15-DEC-1998
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                      burgdorferi.
Nature 390:5
[2]
                                                                               Utterback T., Watthey L., McDonald Garland S., Fujii C., Cotton M.D.,
                                                                                               Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K. Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D., Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman Utterback T., Watthey L., McDonald L., Artiach P., Bowman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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- CAPALYTIC ACTIVITY; ATP + UDP-N-ACETYLMURAMOYL + L-ALL
- ALD + ORTHOPHOSPHATE + UDP-N-ACETYLMURAMOYL-L-ALANINE
- PATHWAY: PEPTIDOGLYCAN BIOSYNTHESIS.
- SUBCELLULAR LOCATION: CYTOPLASMIC (PROBABLE).
- SIMILARITY: BELONGS TO THE MURCDEF FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shigenobu S., Watanabe H., Hattori M., Sakaki Y., "Genome sequence of the endocellular bacterial symBuchnera sp. APS.";
Nature 407:81-86(2000).
                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-ATCC 35210 / B31;
MEDLINE-98065943; PubMed-9403685;
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between the Swiss Institute of Bioinformatics and the EMBL
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MEDLINE=20445173; PubMed=10993077;
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Bacteria; Proteobacteria;
SEQUENCE OF
STRAIN=212;
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                                                                                                                                                                                                                                          Bacteria; Spirochaetales;
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                                                            "Genomic sequence
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                                                                        nd S., Fujii C., Co
H.O., Venter J.C.;
                                   390:580-586(1997).
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71.4%;
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RESULT 14
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GCPE PROTEIN HOMOLOG.
GCPE OR CPN0373 OR CPnach
                                                                                MEDLINE-20150255; PubMed-10684935; Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg White O., Hickey E.K., Peterson J., Utterback T., Berry Linher K., Weidman J., Khouri H., Craven B., Bowman C., Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Eisen J., Fraser C.M.;
     "Genome sequences pneumoniae AR39.";
Nucleic Acids Res.
                                                                                                                                                                                                                                                                                                                                          Kalman S., Mitchell W., Marathe R., Lammel C., Far
Olinger L., Grimwood J., Davis R.W., Stephens R.S.
"Comparative genomes of Chlamydia pneumoniae and C
Nat. Genet. 21:385-389(1999).
                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila
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Pfam; PF00204; DNA_topoisoII; 1.
PRINTS; PR00418; TPI2FAMILY.
PROSITE; PS00177; TOPOISOMERASE_II; 1.
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599 AA; 68774 MW; B5901F17B1CC7721 CRC64;
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28:1397-1406(2000)
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EMBL; AE002246; BAA98581.1; -.
TIGR; CP0383; -.
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                 rattus norv
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| 45 | 44 | 43 | 42 | 41 | 40 | 39 | 38 | 37 | 36 | ω UI | 34 | ω ω | 32 | 31 | 30 | 29 | 28 | 27 | 26 | 25 | 24 | 23 | 22 | 21 | 20 |
|--------|--------|--------|--------------------|--------------------|--------------------|--------|--------|--------|--------|---------|--------|--------------|--------|--------|--------------------|--------------------|--------------------|--------|--------|--------|----------|--------|-------------------|--------|--------------------|
| 31 | 31 | 31 | 31 | 31 | 31 | 31 | 31 | 31 | 31 | 31 | 31 | 31 | 31 | 31 | 31 | 31 | 31 | 31 | 31 | 31 | 31 | 31 | 32 | 32 | 32 |
| • | • | • | • | ٠ | | • | • | • | • | • | ٠ | • | • | • | • | • | • | | • | 73.8 | • | | ٠ | ٠ | |
| 509 | 509 | 497 | 497 | 479 | 465 | 423 | 378 | 339 | 336 | 290 | 276 | 269 | 233 | 232 | 204 | 181 | 178 | 176 | 170 | 146 | 139 | 101 | 666 | 657 | 657 |
| 11 | 11 | 11 | 11 | 11 | N | 10 | σ | 4 | ر. | 4 | 4 | 8 | 10 | 14 | 13 | 4 | 11 | N | 4 | 14 | N | N | υ | 11 | 4 |
| Q9EPI5 | Q9ERZ1 | 088758 | 035173 | Q9EPI4 | 086374 | 049639 | Q9VRC3 | Q9H8E1 | Q9VAI5 | Q9NPS3 | Q9Y4M4 | Q9XLW9 | Q9SI81 | Q9QP22 | Q9PRH7 | Q9NPP3 | 035486 | 087064 | Q9NPM4 | Q9J511 | Q49122 | Q9PH51 | Q9VZX5 | Q9R0C5 | Q9UJ28 |
| rat | | | 035173 mus musculu | Q9epi4 rattus norv | O86374 mycobacteri | w. | | | | homo | | \mathbf{x} | | | Q9prh7 oreochromis | Q9npp3 homo sapien | 035486 mus musculu | | 7 | H | methylob | | Q9vzx5 drosophila | 5 | Q9uj28 homo sapien |

ALIGNMENTS

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               RESULT . 2
065815
   IJ
                                                                                                                                 Query Match
Best Local S
Matches 8
                                                                                                                                                                                                         Genome Res. 0:0-0(2000).
EMBL; U82671; AAF44789.1; -
InterPro; IPR002190; -
Pfam; PF01454; MAGE; 1.
SEQUENCE 314 AA; 34836 M
                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

Mallon A.M., Platzer M., Bates R., Gloeckner G., Botcherby M.,
Mallon A.M., Platzer M., Bates R., Gloeckner G., Botcherby M.,
Nordslek G., Strivens M.A., Kloschis P., Dangel A., Cunningham D.,
Straw R., Weston P., Hunter C., Gilbert M., Fernando S., Goodall K.,
Kerry G., Greystrong J.S., Clark D., Goerdes M., Blechschmidt K.,
Rump A., Hinzmann B., Mundy C.R., Miller W., Poustka A., Herman G.E.,
Rhodes M., Denny P., Rosenthal A., Brown S.D.M.;
"Comparative genome sequence analysis of the Bpa/Str region in mouse
 065815
                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-2000 (Tremblrel. 15, 01-OCT-2000 (Tremblrel. 15, 01-MAR-2001 (Tremblrel. 16, MELANOMA ANTIGEN FAMILY A12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-2000 (TremBLrel.
01-OCT-2000 (TremBLrel.
01-MAR-2001 (TremBLrel.
                                                                                                                                                                                                                                                                                     and man."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MAGEA12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9NSD3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9NSD3
                                                                       1 RIGHLYIL 8
|||||||
171 RIGHLYIL 178
                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
                                                                                                                                   Similarity
8; Conserv
                                                                                                                                   Conservative
 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                            34836 MW;
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100.0%; F
tive 0;
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Last annotation update)
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                                                                                                                                               Score 42;
Pred. No.
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                         7E00F7CECD8F6568 CRC64;
                                                                                                                                   Mismatches
520
                                                                                                                                                             DB 4; Length 314;
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RESULT
Q9VVF8
AC QS
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DT 01
DT 01
DT 02
CG GN CC
GN CO
GN CC
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Best Local
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                                                                                                                                             Q9VVF8 PRELIMINARY;
Q9VVF8;
01-MAY-2000 (TrEMBLrel. 1
01-MAY-2000 (TrEMBLrel. 1
01-MAY-2000 (TrEMBLrel. 1
01-MAY-2010 (TREMBLREL. 1
CG7692 PROTEIN.
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O1-AUG-1998 (TrE
O1-AUG-1998 (TrE
O1-MAR-2001 (TrE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
01-MAR-2001 (TREMBLrel. 16, Last annotation update)
01-AUG-1998 (TREMBLR) (
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CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Magnoliophyta; eudicotyleo euasterids II; Asterales; Helianthus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ANTIMICROBIAL COMPOUNDS OF LEGUMES.

-i- ALTERNATIVE PRODUCTS: TWO FORMS; CYP81B1L (SHOWN HERE)
CYP81B1S; ARE PRODUCED BY ALTERNATIVE SPLICING.
-i- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
EMBL; AJ000478; CAA04117.1; -.
EMBL; AJ000477; CAA04116.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Werck-Reichhart D.; "Cloning, expressio
                         Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc
                                                                                                                       CG7692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NADP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oxidoreductase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001128; -. Pfam; PF00067; p450; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         <del>:</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cabello-Hurtado F., Batard Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-CV. BLANC COMMUN; TISSUE=TUBER; MEDLINE=98184826; PubMed=9516419;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 IGHLYIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AMINOPURINE.

PATHWAY: INVOLVED IN THE BIOSYNTHESIS OF LEGUMES.

ANTIMICROBIAL COMPOUNDS OF LEGUMES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ENZYME REGULATION: ENZYME ACTIVITY IS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PR00385; P450
; PS00086; CYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          expression in yeast, and functional characterization of a plant cytochrome P450 that catalyzes in-chain hydroxyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           456
9
40
51
78
520 l
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Monooxygenase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CYTOCHROME_P450; UNKNOWN_1
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22
40
51
78
58914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      83.3%;
   Endopterygota; Diptera;
ilidae; Drosophila.
                                                                                                                                                                                13,
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MISSING (IN CYP81B1S).

MISSING (IN CAA04116).

Y -> S (IN CAA04116).

P -> Q (IN CAA04116).

P -> Q (IN CAA04116).
                                                                                                                                                                                   Created)
Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score
                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Salaun J.-P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         No. 57;
                                                                                                                                                                                                                                                                                                           1310 AA
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                                                                                                                                                                                   update)
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                               Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ISOFLAVONOID-DERIVED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 520;
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RESULT
Q9S1R5
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RA Baleson K.Y., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Berkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Borkova D., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Cornell J.H., Gu Z., Guan P., Harris M.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp V., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., Liang Y., Lin X.,
RA Merkulov G., Milshia N.V., Mobarry C., Morris J., Moshrefi A.,
RA Melson D.R., Welson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Shue B.C., Siden-Kianos I., Simpson M., Skupski M.P., Smith T.,
RA Syler E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Dan S., Pollard J., Puri Y., Reese M.G.,
RA Williams S.M., Moodage T., Wonley K.C., Mu D., Yang S., Zhou Q., Zheng L.,
RA Zheng X.H., Zhong F.M., Zhong W., Zhong W., Zhon S., Zhon G., Zheng L.,
Ra Zheng X.H., Zhong F.M., Zhong W., Zhon G., Zhon G., Zheng L.,
Ra Zheng X.H., Zhong F.M., Zhong G., Zhon G., Zheng L.,
Ra Zheng X.H., Zhong F.M., Zhong G., Zhon G., Zheng L.,
Ra Shou B. D., Shill M. Shill M. Shill M. Shill H.O.,
Ra Zheng X.H., Zhong F.M., Zhong G., Zhong G., Zhong G., Zhong G., Zhong G., 
RC OCC
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Best Local
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                                                                                                                                                                 Q9S1R5
Q9S1R5;
Q1-MAY-2000 (TrEMBLrel. 1
01-MAY-2000 (TrEMBLrel. 1
01-MAY-2000 (TrEMBLrel. 1
PUTATIVE MEMBRANE PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner R.A., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Abril J.F., Abbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Andrews-Pfannkoch C., Baldwin D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=BERKELEY;
MEDLINE=20196006;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AE003524; AAF49353.1; -. FlyBase; FBgn0036714; CG7692. SEQUENCE 1310 AA; 150503 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Science 287:2185-2195(2000).
Science 287:2185-2195(2000).
                                                                                                      Streptomyces coelicolor. Bacteria; Firmicutes; Ac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=7227;
SEQUENCE FROM STRAIN-A3(2);
                                                            NCBI_TaxID=1902;
                                                                                  Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                     219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                            2 IGHLYIL 8
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                                                                                     Streptomycineae;
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                                                                                                                                                                          PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              83.3%;
85.7%;
                                                                                                           Actinobacteria;
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                                                                                                                                                                                                                                        Created)
                                                                                                                                                                                            Last sequence update)
Last annotation updat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 35; DB 5;
Pred. No. 1.5e+02;
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                                                                                     Streptomycetaceae; Streptomyces.
                                                                                                           Actinobacteridae;
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RESULT
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Best Local
                                                           Submitted (OCT-1998) to the E--
-: SIMILARITY: BELONGS TO ZN-
EMBL; AF096371; AAC62795.1;
InterPro: IPR001584;
InterPro: IPR001878;
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Pfam; PF00098; zf-CCHC; 1.
Pfam; PF00665; rve; 1.
PRINTS; PR00939; C2HCZNFINGER
                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=CV. COLUMBIA;
Geisel C., Smith A., I
"The sequence of A. t!
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01-NOV-1998 (TrE
01-MAR-2001 (TrE
T2L5-9 PROTEIN.
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"A set of ordered cosmids and a detailed genetic a the 8 Mb Streptomyces coelicolor A3(2) chromosome.
Mol. Microbiol. 21:77-96(1996).
EMBL; AL109972; CAB53266.1; -.
EMBL; AL109972; CAB53266.1; -.
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082607;
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T2L5.9.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Brassicales; Brassicaceae; Arabidopsis.
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Bentley S.D., Parkhill J.,
Submitted (AUG-1999) to th
  Zinc-finger.
SEQUENCE 1
                                       SMART; SM00343;
                                                                                                                                                                                                                                     Waterston
                                                                                                                                                                                                                                                         STRAIN=CV.
                                                                                                                                                                                                                                                                                                                         Submitted
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Redenbach M., Kieser H.M., Denapaite
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  AA;
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e EMBL/GenBank/DDBJ databa
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  W.
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Pred. No.
                                                                                                                                                                                                                                                                                                                                             T2L5.";
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C2B34A4A509B5C80
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Score

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RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,

RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,

RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,

RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Feldblyum T.V.,

RA Lin X., Kaul S., Rounsley S.D., Barnstead M.E., Reldblyum T.V.,

RA Lin X., Kason T.M., Bowman C.L., Barnstead M.E., Reldblyum T.V.,

RA Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,

RA Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E.,

RA Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E.,

RA Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,

RA Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,

RA Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,

RA Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,

RA Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,

RA Salzberg S.L., Fraser C.M., Venter J.C.,

RA Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,

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RA Salzberg S.L., Fraser C.M., Venter J., Somerville C.R.,

RA Salzberg S.L., Fraser C.M., Venter J., Somerville C.R.,

RA Salzberg S.L., Fraser C.M., Venter J., Somerville C.R.,

RA Salzberg S.L., Fraser C.M., Venter J., Somerville C.R.,

RA Salzberg S.L., Fraser 
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Best Local
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Q45454;
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01-NOV-1996 (TrEMBLre
01-NOV-1998 (TrEMBLre
pROBABLY POSITIONED I
Bacillus subtilis.
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O9SIM3;
O1-MAY-2000 (TrEMBLrel. 13, Created)
O1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
O1-MAR-2001 (TrEMBLrel. 16, Last annotation update)
PUTATIVE RETROELEMENT POL POLYPROTEIN.
                                                                   SEQUENCE FROM N.A. STRAIN-IF03022;
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Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae; Embryophyta; Trachec
Eukaryota; eudicotyledons; core eudicots;
Magnoliophyta; eudicotyledons; core
MEDLINE=95206941; PubMed=7899081;
Meijer W.J., Venema G., Bron S.;
                                                                                                                                                                        Bacillus/Staphylococcus
NCBI_TaxID=1423;
                                                                                                                                                                                                                                            Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                            Plasmid pTA1060.
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Polyprotein; Zinc-finger.
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(TremBLrel. 01, Last sequence update)
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(TremBLrel. 08 of the downstream ore
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461 AA; 162670 MW;
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                                                                                                                                                                                                        group;
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2; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 34;
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                                                                                                                                                                                                           Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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Nucleic Acids Res. 23:612-619(1995).
EMBL; U32380; AAC44422.1; -.
Plasmid.
SEQUENCE 305 AA.
                                                                                 085748;
085748;
01-NOV-1998
01-NOV-1998
01-MAR-2001
CHEW.
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SIGNAL
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SEQUENCE
                                                                     CHEW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-45H;
STRAIN-45H;
Biro S., Bekesi I., Vitalis S., Szabo G
"A substance effecting differentiation
Purification and properties.";
              Treponema denticola.
Bacteria; Spirochaetales;
NCBI_TaxID=158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (OCT-1998) to the EMBL; AF103943; AAC97368.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Birko Z.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Purification and properties."; Eur. J. Biochem. 103:359-363(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               *Cloning and sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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NCBI_TaxID=1911;
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5; Conservative
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ing of the factor C c
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16,
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                                 Spirochaetaceae; Treponema
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Last sequence update)
Last annotation updat
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Pred. No.
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FACTOR C PROTEIN.
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Best Local Similarity 100
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Greene S.R., Stanm L.V.;
"Treponema denticola Chemotaxis genes.";
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ da
EMBL; AF074950; AAC33469.1; -.
Interpro; IPR000780; -.
Interpro; IPR001601; -.
Interpro; IPR002545; -.
Pfam; PF01594; CheW; 1.
Pfam; PF01799; CheR; 1.
SMART; SM00138; MeTrc; 1.
SMART; SM00138; MeTrc; 1.
SMART; SM00138; MeTrc; 1.
                                                         Pfam; PF00024; PAN; 1.
Pfam; PF00085; kringle; 4.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
PRINTS; PR00018; KRINGLE.
PRODOM; PD000583; -; 1.
PROSITE; PS00021; KRINGLE_1; UNI
PROSITE; PS00070; KRINGLE_2; 4.
                                                                                                                                                                                                                                                                                                                                                    Submitted (DEC-1999) to the F-i-SIMILARITY: TO SERINE PRC-i-SIMILARITY: TO CHYMOTRYPS EMBL; AC004960; AAC71655.1; HSSP; P14210; 1BHT.
                                                                                                                                                                                                                                           InterPro; IPR000001; -.
InterPro; IPR000327; -.
InterPro; IPR001254; -.
InterPro; IPR001314; -.
InterPro; IPR003014; -.
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01-MAR-2001
HEPATOCYTE G
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SEQUENCE FROM D
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Submitted
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01-MAY-2000
  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Courtney L., Elliot G., Angell S.; "The sequence of Homo sapiens PAC clone RP5-11 Submitted (JUN-1998) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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                    Hydrolase;
                                           SMART; SM00020; Tryp_SPc; 1.
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(JUN-1998)
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Serine protease 723 AA; 82602 I
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                                                                                                                                                                                                                                                                                                                                                                                                  9) to the EMBL/GenBank/DDBJ databases
SERINE PROTEASES, TRYPSIN FAMILY.
CHYMOTRYPSIN SERINE PROTEASE FAMILY
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100.0%;
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  WW;
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Pred. No.
                                                                                       UNKNOWN_4
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  627B1EF99FAD931B
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GenBank/DDBJ databases
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Query Match

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Similarity 5; Conserv

62.5%;

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Best Local S
Matches 5
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Q9NP96;
01-CCT-2000 (TTEMBLrel. 15, C
01-CCT-2000 (TTEMBLrel. 15, L
01-MAR-2001 (TTEMBLrel. 16, L
               "The harne 2H9 gene, which is involuntially spliced gene.";
Blochim. Bloophys. Acta 0:0-0(2000).
EMBL; AF13236; AAF68850.1;
EMBL; AF13250; AAF68844.1;
                                                                                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=PLACENTAL ARTERY;
Zheng J., Tsoi S.C., Magness
"Growth factor expression in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ovis aries (Sheep).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrat Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Bovidae; Caprinae; Ovis.
                                                               Honore
                                                                                              Biochim.
                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (MAR-2000) to the EMBL; AF251147; AAF87226.1; InterPro; IPR001664; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-2000 (TrEMBLrel. 15,
01-OCT-2000 (TrEMBLrel. 15,
01-MAR-2001 (TrEMBLrel. 16,
                                                                          SEQUENCE FROM N.A.
                                                                                                             Honore B ;
"The hnRNP 2H9 gene, which is involved
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01-OCT-2000
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MEDLINE=20461765; PubMed=10858537;
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         nterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                         PF00038;
                                                                                                                                                                                                                                                                                                                                      Similarity 83. 5; Conservative
                                                                                           spliced gene.";
Biophys. Acta 1492:108-119(2000)
         IPR000504; -.
                                                                                                                                                                                                                                                                                                                                                                                     154 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                     filament; 1.
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17171 MW;
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Last sequence update)
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                                                                                                                                                                                                                                                                                                                                     Score 32; DB Pred. No. 63; 1; Mismatches
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ovine
                                                                                                                                                                      Craniata; Vertebrata; | Catarrhini; Hominidae;
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                                                    the splicing reaction,
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Best Local
Matches
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STRAIN-DSM 50106;
Bruenker P., Altenbuchner J.;
Submitted (FEB-1998) to the EI
-1- SIMILARITY: BELONGS TO TH
                                                                                                                                                                                                                                                             Q9NPA7;
01-OCT-2000
01-OCT-2000
01-MAR-2001
                                                                                                                                                                 Homo sapiens (Human).
Eukaryota; Metazoa; Ch
Mammalia; Eutheria; Pr
NCBI_TaxID=9606;
                               "The hnRNP 2H9 gene, multiply spliced gene Biochim. Biophys. Act
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-1998
01-JUN-1998
01-MAR-2001
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PROSITE; PS00041; HTH_ARAC_FAMILY_1; 1.

PROSITE; PS01124; HTH_ARAC_FAMILY_2; 1.

SMART; SM00342; HTH_ARAC; 1.

DNA-binding; Transcription regulation.

DNA-binding; Transcription regulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      052770
052770;
 SEQUENCE FROM N.A
                                                                                         Honore
                                                                                                       SEQUENCE FROM N.A.
MEDLINE=20461765; PubMed=10858537;
                                                                                                                                                                                                                                               HNRNP 2H9A.
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InterPro; IPR000005; -.
Pfam; PF00165; HTH_AraC; 1.
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NCBI_TaxID=294;
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Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                         154
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                                                                                             В.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity 62.5 5; Conservative
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Primates;
                                                               which is involved in
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Pred. No. 1
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Catarrhini;
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annotation update)
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annotation
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i; Hominidae; Homo.
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1.3e+02;
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on update)
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Search completed: June Job time: 346 sec
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Best Local S
Matches 6
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Best Local Similarity
Matches 6; Conserv
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MEDLINE-97153147; PubMed-8999868;

Mahe D., Mahl P., Gattoni R., Fischer N., Mattei M.G., Stevenin J.,

Fuchs J.P.;

"Cloning of human 2H9 heterogeneous nuclear ribonucleoproteins.

Relation with splicing and early heat shock-induced splicing arrest.";

J. Biol. Chem. 272:1827-1836(1997).
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"The hnrNP 2H9 gene, which is involved in the splicing reaction, multiply spliced gene.";
Biochim. Biophys. Acta 0:0-0(2000).
EMBL; AF132361; AAF68849.1; -.
EMBL; AF132360; AAF68847.1; -.
InterPro; IPR000504; -.
Pfam; PF00076; rrm; 2.
SEQUENCE 331 AA; 35239 MW; A3BA8D0F5FC07369 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9Y4J5 PRELIMINARY; PRT; 346 AA.
Q9Y4J5,
Q9Y4J5,
Q1-NOV-1999 (TrEMBLrel. 12, Created)
Q1-NOV-1999 (TrEMBLrel. 12, Last sequence update)
Q1-OCT-2000 (TrEMBLrel. 15, Last annotation update)
RIBONUCLEOPROTEIN (HNRNP 2H9).
                                                                                                                                                                                                                                                                                                                                                                                                            multiply spliced gene.";
Biochim. Biophys. Acta 0:0-0(2000).
EMBL; L32610; AAM5179.1; -.
EMBL; AF132360; AAF68843.1; -.
InterPro; IPR000504; -.
Pfam; PF00076; rrm; 2.
Nucleocapsid; Ribonucleoprotein.
SEQUENCE 346 AA; 36926 MW; F7D14C2947930E9E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
HONORE B.;
"The hnRNP 2H9 gene, which is involved
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                                                                                                                                                1 RIGHLYI 7
| | | | | | 1
80 RIGHRYI 86
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85.7%;
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Pred. No. 1.4e+02;
0; Mismatches 1; Indels
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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length: 2000000000
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1: /SIDS6/gcgdata,
2: /SIDS6/gcgdata,
3: /SIDS6/gcgdata,
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Gapop 10.0 , Gapext 0.5
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Copyright (c) 1993 - 2000 Compugen Ltd
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                                                               Y46062
W23043
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R50283
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Jerusalem artichok
MAGE-21 nonapeptid
MAGE-21 nonapeptid
Immunogenic peptid
MAGE-12/HLA-B44 tu
Immunogenic peptid
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| | 45 | 44 | 43 | 42 | 41 | 40 | 9 | ω Θ | 37 | 36 | 35 | 34 | 33 | 32 | 31 | 30 | 29 | 28 | 27 | 26 | 25 | 24 | 23 | 22 | 21 | 20 | 19 | 18 | 17 | 16 | 15 | 14 | 13 | 12 |
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| | R20005 | R15623 | R14243 | R12792 | R10656 | W59923 | W76690 | R99689 | R99688 | R82685 | R57028 | R57027 | R57026 | R29819 | R25677 | R21142 | R15624 | R14307 | R07144 | B45838 | V59030 | Y98485 | Y06593 | Y06589 | Y06591 | в02565 | Y01720 | R25692 | W16330 | W16331 | Y98994 | ā | 08 | Y47357 |
| i | | Hu | Hu | Hu | не | Hu | Hu | TCF | TCF | Tu | Hu | H | Hu | TC | Re | Hu | Hu | וַק | Tu | Z | Se :: | He | Ω. | | E i | ¥ : | Ţ. | CH. | Hı | Ве | н | An . | In | In |
| панан перасосусе у | h | leukocyte- | | hepatocyté | ic parenchym | | an plasm | mutant | mutant having | r cytotoxi | modified | modified t | ild | TCF-II. R29819: | Ę | | | | Tumour cytotoxic f | | f a pen | ブ | | Lipoprotein D-Mage | <u> </u> | Human MAGE-A3 prot | AGE-3 nolvne | XV to X | Human MAGE-3 tumou | ດ | \vdash | O. | | Immunogenic pentid |

ALIGNMENTS

Y05902

Jerusalem artichoke in-chain hydroxylase CYP81B1.

02-AUG-1999 (first entry)

Y05902;

Y05902 standard; Protein; 505

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Batard Y, Benveniste Helvig C, Le Bouquin Werck-Reichhart D;
Nucleic acid encoding plant fatty acid hydroxylases
                  WPI; 1999-264030/22.
N-PSDB; X58406.
                                                                                        06-OCT-1997;
                                                                                                                                                       Helianthus tuberosus.
                                                                                                                                                                       In-chain hydroxylase; transgenic plant; lipid; hydroxylation; oilseed; vegetable oil; crop protection; Jerusalem artichoke; CYP81B1; cytochrome P450.
                                                                        (CNRS ) CENT NAT RECH SCI.
                                                                                                        06-OCT-1998;
                                                                                                                        15-APR-1999.
                                                                                                                                        W09918224-A1.
                                                                                       97US-0060960.
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                                               Cabello-Huartado
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Example 4; Fig

20A-B; 157pp; English

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RESULT RE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence represents in-chain hydroxylase CYP81B1 of Jerusalem artichoke. CYP81B1 is a microsomal cytochrome P450 that C catalyses the omega-2, omega-3 and omega-4 hydroxylation of capric, clauric and myristic acids. The major metabolite is the comega-3 hydroxylated compound. The invention provides isolated nucleic acids (see x58400-06) encoding plant fatty acid nucleic acids (see x58400-06). Also claimed are host cells, transgenic plants and compositions consisting of the plant fatty acid dydroxylase, a process for isolating additional fatty acid hydroxylase genes from a plant, and a process of altering the fatty acid composition in a plant by expressing the plant fatty acid composition in a plant by expressing the plant fatty acid hydroxylase in a transgenic plant, and hydroxylating or epoxidating the fatty acid composition in the plant. Manipulating the hydroxylated attack by insects and other poets. The transgenic plants may also be used as sources of hydroxylated and epoxidized fatty acids useful in the manufacture of e.g. lubricants, anti-slip agents.
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Matches 6
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26-MAR-1993;
07-JUN-1993;
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Disclosure; Page 20;
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                                                                                                                                                                                                                                                                                       Boon-falleur T,
                                                                                                                                                                                                                                                                                                                                        (LUDW-) LUDWIG
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                                                          ew nona:peptide derived from tumour rejection antigen precursor
presented by HLA-Al cancer cells, for use in diagnosis or
herapy of esp. melanoma and breast cancer.
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les 6; Conserv
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93US-0037230.
93US-0073103.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
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RESULT
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Matches 6
antigen region of the full length MAGE sequences. These peptides were used to design the nonapeptides of the invention (see R9937-R99342), which bind to a HLA molecule on a cell, and provoke lysis by cytolytic T cells (CTLs) specific for a complex of the HLA molecule and nonapeptide. The nonapeptides can be used diagnostically to identify tumours expressing a particular HLA molecule, or to identify cancer cells. The peptides can also be used therapeutically to induce a CTL response to tumours (where the peptides are optionally coupled to tumour-specific antibodies), or to induce a response by CTLs that are otherwise inactive. The peptide sequences may also be used to expand specific CTLs in vitro for later return to the patient, such as for treating melanoma. Tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HIA binding peptide; cell lysis; cytolytic T cell; MAGE family; human; tumour rejection antigen precursor; TRA; MAGE-1; tumour; cancer cell; antibody; melanoma; universal effector cell; vaccine; breast cancer; CTL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R99345 standard; Protein; 9 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         involving HLA-Al subtype cancerous cells. The nucleic acid encoding the nonapeptide can be used as a probe to identify tumour cells. This sequence is homologous to the peptide described and is encoded by the MAGE-21 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     An isolated nonapeptide having the amino acid sequence Glu-Val-Asp-pro-Tle-Gly-His-Leu-Tyr is derived from the tumour rejection antigen precursor encoded by the MAGE-3 gene and presented by HLA-AL. The nonapeptide can be used in a vaccine to treat a cancerous condition
                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-AUG-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MAGE-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R99345
                                                                                                                                                                                                                                  New nona:peptide(s) that bind
by specific cytolytic T cells,
tumours and to expand T cells
                                                                                                                                                                                                                                                                                                  WPI; 1996-402317/40.
N-PSDB; T35410.
                                                                                                                                                                                                                                                                                                                                                                                                                         23-FEB-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9626214-A1
                                                                                                                                                                                                        Example 4; Fig 4; 41pp; English.
                                                                                                                                                                                                                                                                                                                                               Romero
                                                                                                                                                                                                                                                                                                                                                               Boon-Falleur T,
                                                                                                                                                                                                                                                                                                                                                                                          (LUDW-) LUDWIG INST CANCER RES.
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100.0%; Pred. No.
tive 0; Mismatc
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                                                                                                                                                                                                                                          in vitro.
                                                                                                                                                                                                                                                     to HLA molecule(s), for diagnosis and
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Den Eynde B,
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Van Der Bruggen
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CC v45390 to y48214 represent specifically claimed immunogenic peptides CC having a human major histocompatibility complex (MHC) Class I (also CC having as human leukocyte antigen (HLA)) binding motif. The immunogenic CC peptides can bind to a specific HLA allele (i.e. HLA-A subtypes CC HLA-2.1, Al, Al. 2 or All. 1 or HLA-B or C) and induce a cytotoxic T cell Cresponse against the antigen from which the peptide is derived. CC control I lymphocytes (CTLS) which destroy antigen-bearing cells are CC normally induced by an antigen in the form of a peptide fragment bound CC or prevent viral important in tumour rejection and in fighting viral CC infections. The peptides are therefore useful therapeutically to treat CC or prevent viral infections and cancers in mammals (especially humans) CC prostate cancer, hepatitis B and C, AIDS, and renal carcinoma. They can be administered as vaccines to elicit an immune response in CC cancer, or used to treat chronic or acute conditions. They are also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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Matches 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and
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                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 54; 150pp; English
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6; Conserva
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3.2e+05;
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                                                          This peptide is a tumour rejection antigen presented by a HLA-B44 comblecule and derived from a MAGE-12 tumour rejection antigen (WE3038-43). Consider tumour rejection antigens (WE3038-43). Consider the bind to HLA-B44 positive cells, making them useful in identifying cells which present HLA-B44 molecules on their surfaces for use in the diagnosis and therapy of cellular abnormalities. The complex of the tumour rejection antigen and HLA comblecule provokes a cytolytic T cell response. The tumour rejection antigens, or complexes of tumour rejection antigens and that HLA-B44, can be used as vaccines to treat disorders characterised by expression of the TRAP molecule such as cancer, especially melanoma. Vaccines can also be prepared from cells which present the tumour rejection antigen/HLA complexes on their surface, such considered the province of the tumour cells which present the tumour rejection antigen/HLA complexes on their surface, such considered the province of the tumour cells which present considered the tumour rejection can also be prepared from cells which present the tumour rejection can also be prepared from their surface, such considered the province can also be prepared from cells which present the tumour rejection can also be prepared from cells which present the tumour rejection can also be prepared from cells which present considered the tumour rejection can also be prepared from cells which present considered the tumour rejection antigen/HLA complexes on their surface, such considered the cons
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                 Tumour rejection antigens presented by molecules - useful to identify HLA-B44 and therapy of cellular abnormalities
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                                       as non-proliferative transfectants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MAGE-12; tumour rejection antigen precursor; TRAP; HLA-B44; human leukocyte antigen B44; cytotoxic T lymphocyte; cancer
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5. 3.2e+05;
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Query Match Best Local

81.0%; Score 34; 100.0%; Pred. No.

DB 18; Length 10; 0.56;

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RESULT
Y46263
                                                                                                    cc v45390 to v488214 represent specifically claimed immunogenic peptides cc having a human major histocompatibility complex (MHC) Class I (also CC known as human leukocyte antigen (HHA) binding motif. The immunogenic ce peptides can bind to a specific HLA allele (1.e. HLA-A subtypes CC HLA-A2.1, A1, A3.2 or A24.1 or HLA-B or C) and induce a cytotoxic T cell cresponse against the antigen from which the peptide is derived.

CC cytotoxic T lymphocytes (CTLs) which destroy antigen-bearing cells are cytotoxic T lymphocytes (CTLs) which destroy antigen-bearing cells are commally induced by an antigen in the form of a peptide fragment bound cc are particularly important in tumour rejection and in fighting viral care particularly important in tumour rejection and in fighting viral confections. The peptides are therefore useful therapeutically to treat cor prevent viral infections and cancers in mammals (especially humans) cc. e.g. prostate cancer, hepatitis B and C, AIDS, and renal carcinoma. CC They can be administered as vaccines to elicit an immune response in conditions as susceptible or otherwise at risk of viral infection or cancer, or used to treat chronic or acute conditions. They are also useful diagnostically, and can be used to induce a cytotoxic T cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and diagnosis of cancers
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                                  response, by contacting a cytotoxic T cell with the peptide e.g. to produce CTLs ex vivo for infusion back into a patient. The polynucleotides encoding the immunogenic peptides are also useful therapeutically and for immunisation as above.
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Best Local S
Matches 6
                           are particularly important in tumour rejection and in fighting viral infections. The peptides are therefore useful thorapeutically to treat or prevent viral infections and cancers in mammals (especially humans) e.g. prostate cancer, hepatitis B and C, AIDS, and renal carcinoma. They can be administered as vaccines to elicit an immune response in individuals susceptible or otherwise at risk of viral infection or cancer, or used to treat chronic or acute conditions. They are also useful diagnostically, and can be used to induce a cytotoxic T cell response, by contacting a cytotoxic T cell with the peptide e.g. to produce CTLs ex vivo for infusion back into a patient. The polynucleotides encoding the immunogenic peptides are also useful therapeutically and for immunisation as above.
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                                                                                                                                                                                                                                             Y45390 to Y48214 represent specifically claimed immunogenic peptides having a human major histocompatibility complex (MIC) Class I (also known as human leukocyte antigen (HLA)) binding motif. The immunogenic peptides can bind to a specific HLA allele (i.e. HLA-A subtypes HLA-A2.1, A1, A3.2 or A24.1 or HLA-B or C) and induce a cytotoxic T cell response against the antigen from which the peptide is derived. Cytotoxic T lymphocytes (CTLS) which destroy antigen-bearing cells are normally induced by an antigen in the form of a peptide fragment bound to a HLA molecule, rather than the intact foreign antigen itself, and to a HLA molecule, rather than the intact foreign antigen itself, and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (EPIM-) EPIMMUNE INC
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|3 ighlyi 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a human leukocyte antigen binding motif #1940.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Celis E,
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                                                  CC Y45390 to Y48214 represent specifically claimed immunogenic peptides CC CC having a human major histocompatibility complex (MHC) Class I (also CK nown as human leukocyte antigen (HLA)) binding motif. The immunogenic CC peptides can bind to a specific HLA allele (i.e. HLA-A subtypes CF HLA-A2.1, A1, A3.2 or A24.1 or HLA-B or C) and induce a cytotoxic T cell cresponse against the antigen from which the peptide is derived. CC Cytotoxic T lymphocytes (CTLS) which destroy antigen-bearing cells are normally induced by an antigen in the form of a peptide fragment bound CC to a HLA molecule, rather than the intact foreign antigen itself, and CC to a HLA molecule, rather than the intact foreign antigen itself, and CC are particularly improvant in tumour rejection and in fighting viral infections. The peptides are therefore useful therapeutically to treat correct or prevent viral infections and cancers in mammals (especially humans) CC e.g. prostate cancer, hepatitis B and C, AIDS, and renal carcinoma. CC Individuals susceptible or otherwise at risk of viral infection or Cancer, or used to treat chronic or acute conditions. They are also cuseful diagnostically, and can be used to induce a cytotoxic T cell cresponse, by contacting a cytotoxic T cell with the peptide e.g. to produce CTLs ex vivo for infusion back into a patient. The cc produce corrections and for immunisation as above.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-DEC-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Y47950 standard; Peptide;
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Query Match Best Local Similarity

78.6%; 100.0%;

Score 33; Pred. No.

DB 20; 3.2e+05;

Length 9;

Query Match
Best Local Similarity
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78.6%; Score 33; ilarity 100.0%; Pred. No. Conservative 0; Mismatc

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RESULT
Y46214
                                         CC v45390 to v48214 represent specifically claimed immunogenic peptides
CC having a human major histocompatibility complex (MEC) Class I (also
CC known as human leukocyte antigen (HLA)) binding motif. The immunogenic
CC peptides can bind to a specific HLA allele (i.e. HLA-A subtypes
CC HLA-A2.1, Al, Al. 2 or A24.1 or HLA-B or C) and induce a cytotoxic T cell
CC response against the antigen from which the peptide is derived.
CC Cytotoxic T lymphocytes (CTLS) which destroy antigen-bearing cells are
CC consmally induced by an antigen in the form of a peptide fragment bound
CC or praticularly important in tumour rejection and in fighting viral
CC infections. The peptides are therefore useful therapeutically to treat
CC or prevent viral infections and canners in mammals (especially humans)
CC e.g. prostate cancer, hepatitis B and C, AIDS, and renal carcinoma.
CC They can be administered as vaccines to elicit an immune response in
CC cancer, or used to treat chronic or acute conditions. They are also
CC useful diagnostically, and can be used to induce a cytotoxic T cell
CC response, by contacting a cytotoxic T cell with the peptide e.g. to
CC produce CTLs ex vivo for infusion back into a patient. The
CC polymucleotides encoding the immunogenic peptides are also useful
CC therapeutically and for immunisation as above.
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Sequence
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Query Match
Best Local S
Matches 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 67; 150pp;
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Conservative
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                 78.6%; Score 33; 100.0%; Pred. No.
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2 IGHLYI 7

Query Match Best Local S Matches 6

Local Similarity les 6; Conserv

78.6%; Score 33; ilarity 100.0%; Pred. No. Conservative 0; Mismatc

Mismatches

DB 20; 0.91;

Length 10; Indels

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                                                                                       Sequence
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100.0%; Pred. No. 0.
tive 0; Mismatches
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Best Local
                                                                                                                                                                                                                                                                                                                        B08827-37 represent melanoma associated antigen (MAGE)-3 derived immunogenic peptides. The peptides are capable of binding to major histocompatibility complex (MHC) class II molecules. Stimulation with the peptides induces proliferation of CD4+ T cells, and of their cytolytic activity. CD4+ T cells exposed to the peptides were able to cause lysis of melanoma cells expression MAGE-3 and HLA-DR molecules. The peptides are useful for inducing an immune response against tumour cells expressing a MAGE-3 antigen. They are also useful for the preparation of anti-tumour medicament for use as a vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Melanoma associated antigen-3; MAGE-3; immunogenic peptide; major histocompatibility complex; MHC; class II molecule; tumour; CD4+ T cell proliferation; melanoma cell; immune response; vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI;
        Human leucocyte antigen; HLA class II; antigen epitope; pharmaceutical; immune response; chronic viral disease; cancer; autoimmune disease; rheumatoid arthritis; multiple sclerosis; myasthenia gravis; AIDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel melanoma associated antigen (MAGE)-3 derived immunogenic peptides
ellograft
                                                           HLA class
                                                                                   07-AUG-2000
                                                                                                          Y98994;
                                                                                                                                 Y98994 standard;
                                                                                                                                                                                                                                                                                                    Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FOND CENT SAN RAFFAELE DEL MONTE TABOR
                                                                                                                                                                                                                                                                                                                                                                                                                                              Page 18;
 rejection;
                                                         II binding antigen epitope peptide #183.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     vaccine
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                                                                                                                                 Peptide;
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allergy;
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lyme disease; hepatitis;
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prostate cancer;
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                                                                                                                                                                                                              CC diseases (rheumatoid arthritis, multiple sclerosis, and myasthenia CC diseases (rheumatoid arthritis, multiple sclerosis, and myasthenia CC gravis), allograft rejection, allergies, lyme disease, hepatitis, CC post-streptococcal endocarditis or glomerulonephritis and food post-streptococcal endocarditis or glomerulonephritis and food composes against other immunogens administered with the peptides. CC hypersensitivities. The peptide epitopes can be used to enhance immune cresponses spainst other immunogens administered with the peptides. CC plaeases which can be treated using immunogenic mixtures include prostate cancer, hepatitis B, hepatitis C, AIDS, renal carcinoma, cervical coarcinoma, lymphoma, and condyloma acuminatum. The peptides may also be used to make monoclonal antibodies useful as potential diagnostic or therapeutic agents. The peptides may also be useful as diagnostic or treatment regimen. Also, the peptides may be used to predict which individuals will be at substantial risk of developing chronic infection. The selection of appropriate T and B cell epitopes should allow the cavelopment of epitope based vaccines particularly towards conserved correlations of pathogens which are characterized by high sequence
                                                                              Matches
                                                                                                 Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       are derived from various antigens for various human leucocyte antigen class DR molecules, representative of the world wide population. The peptide/analogue binds to an HLA class II molecule at an IC-50 of less than or equal to 1,000 nM. The pharmaceutical can be used to induce a than or equal to 1,000 nM. The pharmaceutical can be used to induce a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   glomerulonephritis; food hypersensitivity; malaria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 than or equal to 1,000 nM. The pharmaceutical can be used to induce a helper T cell response. The pharmaceutical focuses the immune response towards selected determinants and could therefore be used in cases of chronic viral diseases and cancer. Examples of diseases that can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unidentified
                                                                                                                                                                                Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New compositions containing immunogenic peptide epitopes for various HLA class II DR molecules useful for inducing helper T cell response
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               comprising a unit dose form of a peptide,
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                                                                              Similarity 6; Conserv
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Copyright (c) 1993 - 2000 Compugen Ltd.
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SYH_METTH
MURC_BUCAI
SYPC_YEAST
PARE_BORBU
AT1D_HUMAN
RPOB_RICPR
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UPP_MYCDN
Y077_HAEIN
PQQB_ACICA
MAG6_HUMAN
TGT_ARCFU
SYH_METJA
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SNC1_HUMAN
ROF_HUMAN
CDS1_ARATH
ROH1_HUMAN
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OC Mammal
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MAGC_HUMAN STANDARD,
P43365;
O1-NOV-1995 (Rel. 32, Created)
O1-NOV-1995 (Rel. 32, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                             CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE-94102805; PubMed-8276455;
de Smet C., Lurquin C., van der Bruggen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo saplens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Boon T.;
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                                                                                                                DOMAIN
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                                                                                                                                Tumor antigen.
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CC14_YEAST
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RPOL_BPK11
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3F0787CECD8816A5 CRC64;
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                                                                                                                                                                                                                                                                                 This SWISS-PROY entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=20330349; PubMed=10871362; Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K., Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.; "Comparison of whole genome sequences of Chlamydia pneumoniae J138 from Japan and CWL029 from USA."; Nucleic Acids Res. 28:2311-2314(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=20150255; PubMed=10684935;
Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg
White O., Hickey E.K., Peterson J., Utterback T., Berry
Linher K., Weidman J., Khouri H., Craven B., Bowman C.,
Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G.,
Eisen J., Fraser C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-99206606; PubMed=10192388; Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W., Olinger L., Grimwood J., Davis R.W., Stephens R.S.; "Comparative genomes of Chlamydia pneumoniae and C. trachomatis."; Nat. Genet. 21:385-389(1999).
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01-OCT-2000 (Rel. 40, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
01-OCT-2000 (Rel. 40, Last annotation update)
GCPE PROTEIN HOMOLOG.
GCPE OR CPN0373 OR CP0383.
                                                                                                                                                                               EMBL; AE001621; AAD18517.1;
EMBL; AE002200; AAF38230.1;
EMBL; AP002546; BAA98581.1;
TIGR; CP0383; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pneumoniae AR39.";
Nucleic Acids Res.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chlamydia pneumoniae (Chlamydophila pneumoniae). Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Genome sequences of Chlamydia trachomatis pneumoniae AR39.";
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                     VRIGHLYI 8
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Similarity 100.
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                                                                                                                                                                68308 MW;
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Pred. No. 0.(
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17;
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AC P94280
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DT DA GYRB.
OS Barton
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HGF_HUMAN
ID HGF_HUMAN
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VARIANT
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PROSITE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bartonella bacilliformis.
Bacteria; Proteobacteria; alpha subdivision;
Bartonellaceae; Bartonella.
NCBI_TaxID=774;
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15-DEC-1998 (Rel. 37,
01-OCT-2000 (Rel. 40,
DNA GYRASE SUBUNIT B (
                                                                                                                                                                                                                                                                                                                                                                                                                                      Topoisomerase;
VARIANT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001241; -.
InterPro; IPR002288;
Pfam; PF00986; DNA_GYTaseB_C;
Pfam; PF00204; DNA_topoisoII;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mutations in Bartonella bacilliformis gyrB confer
                                                                                                                                                                                                        1 VRIGHLYI 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CATALYTIC ACTIVITY: ATP-DEPENDENT BREAKAGE, PASSAGE OF DOUBLE-STRANDED DNA.

SUBUNIT: MADE UP OF TWO CHAINS. THE A CHAIN IS RESPO BREAKAGE AND REJOINING; THE B CHAIN CATALYZES ATP HY ENZYME FORMS AN A2B2 TETRAMER.

SIMILARITY: BELONGS TO TYPE II TOPOISOMERASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION: DNA GYRASE NEGATIVELY SUPERCOILS CLOSED CIRCULAR DOUBLE STRANDED DNA IN AN ATP-DEPENDENT MANNER AND ALSO CATALYZES THE INTERCONVERSION OF OTHER TOPOLOGICAL ISOMERS OF DOUBLE-STRANDED DNA RINGS, INCLUDING CATENANES AND KNOTTED RINGS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRO0418; TPI2FAMILY.
; PS00177; TOPOISOMERASE_II; 1.
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5; Conserv
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184
214
214
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4 124
G -> S (IN COUMERMYCIN A1 MUTANT).

4 184
R -> Q (IN COUMERMYCIN A1 MUTANT).

4 214
T -> A (IN COUMERMYCIN A1 MUTANT).

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T -> I (IN COUMERMYCIN A1 MUTANT).

5 AA; 77445 MW; F54948EEF342281F CRC64;
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                                                              STANDARD;
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sequence
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Pred. No.
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Mismatches
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HGF OR HPTA.
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Biochem.
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MEDLINE-91025062; PubMed-2145836;
MEDLINE-11. Sugimura A., Shimonishi M., Nishizawa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EQUENCE FROM N.A.
MEDLINE-91340155; PubMed-1831432;
MEDLINE-91340155; PubMed-1831432;
MEDLINE-91340155; PubMed-1831432;
MEDLINE-91340155; PubMed-1831432;
MEDLINE-91340155; PubMed-1831432;
MEDLINE-91340155; PubMed-1831432;
                                                                                                                                                                                                                                                                                      TISSUE-Embryonic fibroblast;
MEDLINE-91334393; PubMed=1831266;
Weidner K.M., Arakaki N., Hartmann G.,
Rieder H., Fonatsch C., Tsubouchi H.,
                                                                                                                                                                                                                                                                                                                                                   Nature
[5]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seki T., Hagiya M., Shimonishi M., Na) "Organization of the human hepatocyte Gene 102:213-219(1991).
                                                                                                                                                                                                                                                                                                                                                                     Nakamura T., Nishizawa T., Hagiya M.
Sugimura A., Tashiro K., Shimizu S.,
"Molecular cloning and expression of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-89392017; PubMed-2528952; Miyazawa K., Tsubouchi H., Naka D., Arakaki N., Nakayama H., Hirono S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
MUTAGENESIS.
MEDLINE-92331602; PubMed-1321034;
Lokker N.A., Mark M.R., Luis E.A.
Baker J.B., Godowski P.J.;
                                                                                                 Shimizu N., Hara H.,
                                                                                                                                                                            Yoshiyama Y., Arakakai N., Naka
Nakayama H., Gohda E., Kitamura
Hishida T., Daikuhara Y.;
                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 growth factor.
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SEQUENCE FROM N.A.
                                                       Biochem.
                                                                                        Nakamura
                                                                                                             MEDLINE-93129192;
                                                                                                                         CARBOHYDRATE-LINKAGE
                                                                                                                                                      "Identification of the N-terminal residue of the heavy chain native and recombinant human hepatocyte growth factor.";
                                                                                                                                                                                                               MEDLINE-91207365;
                                                                                                                                                                                                                           SIGNAL
                                                                                                                                                                                                                                                         hepatocyte
                                                                                                                                                                                                                                                            "Evidence for the identity of human benatocyte growth factor.";
                                                                                                                                                                                                                                                                                Birchmeier
                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-90066676; PubMed=2531289;
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                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seki T., Ihara I., Sugimura A., Shimonishi M., N
Asami O., Hagiya M., Nakamura T., Shimizu S.;
"Isolation and expression of cDNA for different
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Molecular cloning and sequence analysis of cDNA growth factor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human)
                                                                          "Hepatocyte growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E., Daikuhara Y.,
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                                                                                        Shimizu
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nys. Res. Commun. 172:321-327(1990).
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S.;
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Commun. 175:660-667(1991).
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           E.A.,
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Hishida T., Daikuhara Y.,
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X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 35-210.

MEDLINE-99036858; PubMed-9817840;

Ultsch M., Lokker N.A., Godowski P.J., de Vos A.M.;

"Crystal structure of the NK1 fragment of human hepatoc;
factor at 2.0-A resolution.";

Structure 6:1383-1393(1998):

-!- FUNCTION: HGF IS A POTENT MITOGEN FOR MATURE PARENC!

HEPATOCYTE CELLS, SEEMS TO BE AN HEPATOTROPHIC FACTO
AS GROWTH FACTOR FOR A BROAD SPECTRUM OF TISSUES ANITH HAS NO DETECTABLE PROTEASE ACTIVITY.

-!- SUBUNIT: DIMER OF AN ALPHA CHAIN AND A BETA CHAIN L.
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STRUCTURE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Structure-function analysis of hepatocyte growth factor: identification of variants that lack mitogenic activity yet high affinity receptor binding."; EMBO J. 11:2503-2510(1992).
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                DISULFIDE BOND.
SIMILARITY: CONTAINS 4 KRINGLE REGIONS
SIMILARITY: BELONGS TO PEPTIDASE FAMIL-
TRYPSIN FAMILY. PLASMINOGEN SUBFAMILY.
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entities requires or send an email t the European Bioinformatics Institute. The second of the s between SWISS-PROT entry is copyright. non-profit institutions as rong and this statement is not removed. email to Swiss Institute license agreement (See http://www.isb-sib.ch/announce/ license@isb-sib.ch). yright. It is produced through a of Bioinformatics and the EMBL There are no rest Usage restrictions and EMBL for collaboration in no way no

InterPro; IPR000 InterPro; IPR001 InterPro; IPR001 InterPro; IPR003 Pfam; PF00024; I L; M73239; AAA642 L; M73240; AAA642 J10579; J10579; S06794; S06794 2HGF; 24-JUN-98 1BHT; 18-NOV-98 142409; D90325; D90326; D90327; D90328; D90329; D90330; D90334; D90318; D90319; D90333; D90332; D90324; S01.976; IPRO00001; -., IPRO01254; -., IPRO01314; -., IPRO03014; -., teDB; 24-JUN-98. 18-NOV-98. BAA14348.
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PROSITE; PS00021; KRINGLE_1; 4.
PROSITE; PS50070; KRINGLE_2; 4.
Growth factor; Kringle; Glycoprotein;
                                                                                                                                                                                                                                                              HGF_MOUSE STANDARD; PRT; 728 AA. Q08048; Q64007; Q61662; Q1-NOV-1995 (Rel. 32, Created) Q1-NOV-1995 (Rel. 32, Last sequence update) Q1-OCT-2000 (Rel. 40, Last annotation update) HEPATOCYTE GROWTH FACTOR PRECURSOR (SCATTER F.
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               TISSUE-Mammary fibroblast;
MEDLINE-94183257; PubMed-8135822;
Sasaki M., Nishio M., Sasaki T., Enami J.;
Sidentification of mouse mammary fibroblast-derived factor as hepatocyte growth factor. 772-772/1864)
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Mammalia; Eutheri
NCBI_TaxID=10090;
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     199:772-779(1994)
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-!- FUNCTION: HGF IS A P
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MEDLINE=94060105; PubMed=8241272;
Liu Y., Michalopoulos G.K., Zarnegar
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ALTERNATIVE PRODUCTS: A SF
ALTERNATIVE RNA SPLICING.
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CHAIN. BLOPHYS. ACTA 1216:299-303(1993).

FUNCTION: HGF IS A POTENT MITOGEN FOR MATURE PARENCHYMAL HERATCOYTE CELLS, SEEMS TO BE AN HERATCOTOPHIC FACTOR, AN AS GROWTH FACTOR FOR A BROAD SPECTRUM OF TISSUES AND CELL IT HAS NO DETECTABLE PROTEASE ACTIVITY.

SUBUNTY: DIMER OF AN ALPHA CHAIN AND A BETA CHAIN LINKED
                                            s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EM European Bioinformatics Institute. There are no restr by non-profit institutions as long as its content
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SIMILARITY: CONTAINS 4 KRINGLE REGIONS
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InterPro; IPR001314; -
InterPro; IPR003014; -
Pfam; PF00024; PAN; 1
Pfam; PF00051; kringle; 4
Pfam; PF00089; trypsin; 1
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SERINE PROTEASE-LIKE.

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A OKAJINA A., MAYAZAWA K., KITAMURA M., A OFTA CHANA A.,

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                                   EMBL; D90102; BAA14133.1; -
EMBL; X54400; CAA38266.1; -
PIR; S13211; S13211.
PIR; A35644; A35644.
HSSP; P14210; 2HGF.
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01-NOV-1990 (Rel. 16, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
HEPATOCYTE GROWTH FACTOR PRECURSOR (SCATTER FACTOR) (SF)
(HEPATOPOEITIN A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HGF_RAT P17945;
                                                                                                                                                     the European Bioinformatics Institute. The use by non-profit institutions as long a modified and this statement is not removed. entitles requires a license agreement (See lor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Deduced primary structure of rat hepatocyte grow expression of the mRNA in rat tissues."; Proc. Natl. Acad. Sci. U.S.A. 87:3200-3204(1990).
                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TEQUENCE FROM N.A.

CHENTN-WISTAR; TISSUE-Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A., AND PARTIAL S
STRAIN-WISTAR; TISSUE-Liver;
MEDLINE-90222197; PubMed-2139229;
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Mammalia; Eutheria;
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Rattus norvegicus (Rat).
Metazoa; Chordata;
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    InterPro;
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S., Nakamura T.;
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    IPR000001;
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Pred. No. 31;
3; Mismatches
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Sciurognathi; Muridae;
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InterPro; IPR003014; -.
InterPro; IPR003014; -.
Pfam; PF00024; PAN; 1
Pfam; PF00025; kringle; 4
Pfam; PF00089; kringle; 1
Pfam; PF00018; kringle.
PRINTS; PR00018; KRINGLE.
PRINTS; PR00722; CHYMOTRYPSIN.
PROSITE; PS00071; KRINGLE.1; 4
PROSITE; PS00070; KRINGLE.2; 4
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Mammalia; Eutheria;
NCBI_TaxID=9606;
                                                                                                                                                       MUTAGENESIS.
TISSUE=Blood;
                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE-94102805; PubMed-8276455;
de Smet C., Lurquin C., van der B
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  DEVELOPMENT AND TUMOR
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s 39:121-129(1994).
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Primates;
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Gaugler B., van den Eynde B., van der Brugaforio J.J., de Plaen E., Lethe B., Bras "Human gene MAGE-3 codes for an antigen raturologous cytolytic T lymphocytes."; J. Exp. med. 179:921-930(1994).
                                                                                                                                                                                                                                                                                                                                                             MAG2_HUMAN STANDARD; PRT; 314 AA P43356; O1-NOV-1995 (Rel. 32, Created) O1-NOV-1995 (Rel. 32, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation updat MELANOMA-ASSOCIATED ANTIGEN 2 (MAGE-2 ANTIG MAGEA2 OR MAGE2.
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KRINGLE 1.

KRINGLE 2.

KRINGLE 3.

KRINGLE 4.

SERINE PROTEASE-LIKE.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                Bruggen
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Brasseur
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ANTIGEN)
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A ROLE IN EMBRYONAL OR ASPECTS OF TUMOR
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Query Match
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                                                                             MEDLINE-94311935; PubMed=8037761;

Ding M., Beck R.J., Keller C.J., Fenton R.G.;

Pioning and analysis of MAGE-1-related genes.";

Biochem. Biophys. Res. Commun. 202:549-555(1994).

-!- FUNCTION: NOT KNOWN, THOUGH MAY PLAY A ROLE IN EMBRYONAL-
-!- PUNCTION: NOT KNOWN, THOUGH MAY PLAY A ROLE IN EMBRYONAL-
-!- PECHOPMENT AND TUMOR TRANSFORMATION OR ASPECTS OF TUMOR PROGRESSION. ANTIGEN RECOGNIZED ON A MELANOMA BY AUTOLOGY

CYTOLYTIC T LYMPHCYTES.
                                                                                                                                                                                                                                                                                                                Gaugler B., van den Eynde B., van der Bruggen P., I Gaforio J.J., de Plaen E., Lethe B., Brasseur F., E "Human gene MAGE-3 codes for an antigen recognized autologous cytolytic T lymphocytes.";

1. Exp. Med. 179:921-930(1994).
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P43357;
01-NOV-1995 (Rel. 32, Created)
11-NOV-1995 (Rel. 32, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
MELANOMA-ASSOCIATED ANTIGEN 3 (MAGE-3 ANTIGEN) (ANTIGEN MZ2-D).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antigen; Multigene family; Tumor antigen.
DOMAIN 40 43 POLY-SER,
MUTAGEN 170 170 V->D: IMPROV
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                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=94157413; PubMed=8113684;
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TISSUE SPECIFICITY: EXPRESSED IN MANY TUMORS OF SEVERAL TYPES, SUCH AS MELANOMA, HEAD AND NECK SQUAMOUS CELL CARCINOMA, LUNG CARCINOMA AND BREAST CARCINOMA, BUT NOT IN NORMAL TISSUES EXCEPT FOR TESTES.
  TISSUE SPECIFICITY: EXPRESSED IN MANY TUMORS OF SEVERAL TYPES, SUCH AS MELANOMA, HEAD AND NECK SQUAMOUS CELL CARCINOMA, LUUG CARCINOMA, AND BEAST CARCINOMA, BUT NOT IN NORMAL TISSUES EXCEPT FOR TESTES AND PLACENTA. NEVER EXPRESSED IN KIDNEY TUMORS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WITH MAGE-12.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IPR002190; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             314 AA;
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77.88;
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Pred. No. 21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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Boon T.;
d on a melanoma
                                           SEVERAL TYPES, ARCINOMA, LUNG
                                                                                                          AUTOLOGOUS
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RESULT 9
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Best Local S
Matches 6
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Q91754;
Q1-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOY-1997 (Rel. 35, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
GLUCOKINASE REGULATORY PROTEIN (GLUCOKINASE REGULATOR).
Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                              phosphate-insensitive regulatory protein of glucokinase.";
Eur. J. Biochem. 225:43-51(1994).
-i- FUNCTION: INHIBITS GLUCOKINASE BY FORMING AN INACTIVE COMPLEX WITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MIM;
               PROSITE;
                                                                                                                                                                                                                                                                                                                                          TISSUE=Liver;
MEDLINE=95010134; PubMed=7925465;
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                            Pfam; PF01380;
                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MUTAGEN
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                                                                             EMBL; X80901; CAA56863.1;
                                                                                                                                                                                                                                    <u>-</u>
                                                                                                                                                                                                                                                                                                             Veiga-Da-Cunha M., Detheux M., Watelet N., van Schaftingen Cloning and expression of a Xenopus liver cDNA encoding a
                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                         Xenopodinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    <del>-</del>
                                             interPro; IPR001347;
interPro; IPR001741;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nterPro; IPR002190; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               172 IGHLYI 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 IGHLYI 8
                                                                                                                                                                                                                                  SIMILARITY: BELONGS TO THE SIS FAMILY. GCKR SUBFAMILY
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               PS01272;
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176
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(Rel. 35, Last sequence up
(Rel. 39, Last annotation
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                               SIS;
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GCKR; 1.
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Pred. No.
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 41B72C1981D1BA52 CRC64;
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Conservative

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                                                                                                                                                                                                                                                                                                                                                                                                                      PROTEIN.";
Plant Physiol. 100:1787-1795(1992).
Plant Physiol. CHANNEL PROTEIN IN TONOPLAST. THESE PROTEINS MAY ALITHE DIFFUSION OF AMINO ACIDS AND/OR PEPTIDES FROM THE TONOPLAY.
INTERIOR TO THE CYTOPLASM.
-I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-I- TISSUE SPECIFICITY: FOUND IN ALL SEED TISSUES THAT ARE ALIVE SEED MATURITY, BUT NOT IN TISSUES THAT LOSE VIABILITY DURING SEED MATURITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TIPA_PHAVU STANDARD; PRT; 256 AA.

P23958;
01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 22, Last sequence update)
01-JUL-1993 (Rel. 26, Last annotation update)
TONOPLAST INTRINSIC PROTEIN, ALPHA (ALPHA TIP).
Phaseolus vulgaris (Kidney bean) (French bean).
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
Fabaceae; Papillionoideae; Phaseolus.
                              TRANSMEM
DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A., AND SEQUENCE OF 11-21.
STRAIN-CV. GREENSLEEVES; TISSUE-Seed;
MEDLINE-93044451; PubMed-2152174;
                                                                                                                                                                                                         PIR; JQ1106; JQ1106.
PIR; S26742; S26742.
InterPro; IPR000425;
                                                                                                                                                                                                                                                                            entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                    PRINTS; PR00783; MINTRINSICP. PROSITE; PS00221; MIP; 1.
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                                                                                                                                                                   PROSITE;
                                                                                                                                                                                               Pfam; PF00230; MIP; 1.
                                                                                                                                                                                                                                                                                                        modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Tonoplast-bound protein kinase phosphorylates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Johnson K.D.,
     DOMAIN
                                                          DOMAIN
                                                                                                                                                       Transport;
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                                                                                                                                                                                                                                                                                                                  ween the Swiss Institute of Bioinformatics
European Bioinformatics Institute. There a
by non-profit institutions as long as i
                                                                                                                                                                                                                                                                                                                                                                                                                PTM: PHOSPHORYLATED BY A TONOPLAST-BOUND CALCIUM-DEPENDENT
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CYTOPLASMIC (POTENTIAL)
POTENTIAL.
CYTOPLASMIC (POTENTIAL)
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VACUOLAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL)
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DOMAIN
MOD_RES
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Q16533;
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                                                                                                                                                                                                              30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
30-MAY-2000 (Rel. 39, Last annotation update)
SURINA ACTIVATING PROTEIN COMPLEX 43 KDA SUBUNIT (SNAPC 43 KDA SUBUNIT) (PROXIMAL SEQUENCE ELEMENT-BINDING TRANSCRIPTION FACTOR SUBUNIT) (PSE-BINDING FACTOR GAMMA SUBUNIT) (PTF GAMMA SUBUNIT).
                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collat between the Swiss Institute of Bioinformatics and the EMBL outsit the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified and this statement is not removed. Usage by and for commodified and this statement is not removed.
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                                                 EMBL; Z47542; CAA87590.1;
EMBL; U44754; AAC50358.1;
MIM; 600591;
            Transcription regulation. DOMAIN 347 352
                                                                                               entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=96104548; PubMed=8524284;
Yoon J.B., Roeder R.G.;
                                                                                                                                                                                                                                                                                                                                                                                             RNA polymerase II and III Nature 374:653-656(1995).
                                                                                                                                                                                                                                                                                                                                                                                                       Henry R.W., Sadowski C.L., Kobayashi R., Herna
"A TBP-TAF complex required for transcription
RNA polymerase II and III.";
                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A., AND PARTIAL SEQUENCE MEDLINE=95231630; PubMed=7715707;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human)
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 SEQUENCE
                                     TRANSFAC; T01680;
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 368 AA;
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256
42994 MW;
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CYTOPLASMIC (POTENTIAL).
PHOSPHORYLATION (BY CDPK) (PROBABLE).
7862A0AC8EB46810 CRC64;
POLY-GLU.
; 324E89CF8B540C32 CRC64;
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ption of human
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Matunis M.J., Xing J., Dreyfuss G.;
"The hnrNP F protein: unique primary structure, properties, and subcellular localization.";
Nucleic Acids Res. 22:1059-1067/1004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-96081943; PubMed-7499401;
HONDIE B., RASMUSSEN H.H., VORUM H., Dejgaard K., Liu X.,
Gromov P., Madsen P., Gesser B., Tommerup N., Celis J.E.;
"Heterogeneous nuclear ribonucleoproteins H, H', and F are members of
a ubiquitously expressed subfamily of related but distinct proteins
encoded by genes mapping to different chromosomes."
J. BIOL. Chem. 270:28780-28789(1995).
-!- FUNCTION: THIS PROTEIN IS A COMPONENT OF THE HETEROGENOUS NUCLEAR
RIBONUCLEOPROTEIN (HNRNP) COMPLEXES WHICH PROVIDE THE SUBSTRATE
FOR THE PROCESSING EVENTS THAT PRE-MRNAS UNDERGO BEFORE BECOMING
FUNCTIONAL, TRANSLATABLE MRNAS IN THE CYTOPLASM. PROBABLY BINDS G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last seq
01-OCT-2000 (Rel. 40, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Aarhus/Ghent-2DPAGE;
Aarhus/Ghent-2DPAGE;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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hes 6; Conserv
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SUBCELLULAR LOCATION: NUCLEAR; NUCLEOPLASM.
TISSUE SPECIFICITY: EXPRESSED UBIQUITOUSLY.
SIMILARITY: CONTAINS 3 RNA RECOGNITION MOTIFS (RRM).
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   RIGHLYI 8
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                                                                                                                                                          D30076; rim, ...

PS50102; RRM, RNP_1; FALSE_NEG.

PS00030; RRM_RNP_1; FALSE_NEG.

Protein; RNA-Binding; Ribonucleoprotein; Repeat.

RNA-BINDING (RRM) 1.

11 188 RNA-BINDING (RRM) 2.

111 188 RNA-BINDING (RRM) 3.

289 366 RNA-BINDING (RRM) 3.
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Rel. 40, Last annotation update)
NUCLEAR RIBONUCLEOPROTEIN F (HNRNP
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7312;
                                                                                   69.6%;
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                                                          Score 32; DB; Pred. No. 44; 0; Mismatches
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                                                                                                                  Length 415;
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CDS1_ARATH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cheuk R., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson Khan S., Kim C., Altafi H., Bei B., Chin C., Chiou J., Choi E., Connay A., Gonzalez A., Hansen N., Howing B., Koo T., Lam Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsky N., Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N. Theologis A., Ecker J.;
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
-i- PUNCTION: MAY BE INVOLVED IN THE SYNTHESIS OF MINOR PHOSPHOLIPI AND IN MODULATION OF IP3-MEDIATED SIGNAL TRANSDUCTION.
-i- CATALTIC ACTIVITY: CTP + PHOSPHATIDATE = PYROPHOSPHATE +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDS1_ARATH STANDARD; PRT; 4/1 AA. 004928; 048808; 15-JUL-1998 (Rel. 36, Created) 15-JUL-1998 (Rel. 36, Last sequence update) 15-JUL-1998 (Rel. 40, Last annotation update) D1-OCT-2000 (Rel. 40, Last annotation update) PHOSPHATIDATE CYTIDYLYLTRANSFERSE (EC 2.7.7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Magnoliophyta; eudicotyledons; core eudicots; Brassicales; Brassicaceae; Arabidopsis. NCBI_TaxID-3702;
                                                                                                                         TRANSMEM TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Kopka J., Ludewig M., Mueller Roeber B.;
"Complementary DNAs encoding eukaryotic-type cytidine-5'-diphosphate-
diacylglycerol synthases of two plant species.";
Plant Physiol. 113:997-1002(1997).
                                                                                                                                                                                                                                                                                                                               EMBL; X94306; CAA63969.1; -. EMBL; AC003113; AAF70845.1; -. Mendel; 27238; Arath;2834;27238
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STRAIN=CV. C24; TISSUE-Flower,
                                                            TRANSMEM
                                                                                                                                                                                                                  Transferase;
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                                                                                               TRANSMEM
                                                                                                                                                                                     Transmembrane
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SUBCELLULAR LOCATION: INTEGRAL MEMBRAN
SIMILARITY: BELONGS TO THE CDS FAMILY.
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   421 AA;
                                                            149
206
246
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Ouery Match
Best Local Similarity 75.
Matches 6; Conservative

69.6%;

Score 32; DB Pred. No. 45; 1; Mismatches

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Length 421;

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                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformaticy Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Microsequences of 145 proteins recorded in the two-dimensional protein database of normal human epidermal keratinocytes."; Electrophoresis 13:960-969(1992).

-i- FUNCTION: THIS PROTEIN IS A COMPONENT OF THE HETEROGENOMES NO
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Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia: Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                            Aarhus/Ghent-2DPAGE: 4410;
Aarhus/Ghent-2DPAGE: 4429;
Aarhus/Ghent-2DPAGE: 5416;
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"The hnRNP F protein: unique primary structure,
properties, and subcellular localization.";
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01-OCT-2000
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P31943;
    PROSITE; PS00030; RRM_RNP_1; FALSE_NEG Nuclear protein; RNA-binding; Ribonucle
                                                                                                                                                                                                                                                                                                                                                            EMBL; L22009; AAA91346.1; -
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MEDLINE-93162043; PubMed-1286667;
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                                                                                                                        Pfam; PF00076;
                                                                                                                                                           InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION: THIS PROTEIN IS A COMPONENT OF THE HETEROGENOUS NUCLEAR RIBONUCLEOPROTEIN (HRNNP) COMPLEXES WHICH PROVIDE THE SUBSTRATE FOR THE PROCESSING EVENTS THAT PRE-MRNAS UNDERGO BEFORE BECOMING FUNCTIONAL, TRANSLATABLE MRNAS IN THE CYTOPLASM. BINDS POLY (RG). SUBCELLULAR LOCATION: NUCLEAR; NUCLEOPLASM.
TISSUE SPECIFICITY: EXPRESSED UBIQUITOUSLY.
TISSUE SPECIFICITY: EXPRESSED UBIQUITOUSLY.
DOMAIN: EACH QUASI-RRM REPEAT BOUND POLY(RG), WHILE ONLY THE N-TERMINAL QRAM BOUND POLY(RC) AND POLY (RQ). NONE OF THE REPEATS BOUND DETECTABLE AMOUNTS OF POLY (RA).
SIMILARITY: CONTAINS 3 RNA RECOGNITION MOTIFS (RRM).
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                                                                                      PS50102; RRM;
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(Rel. 34, Last sequence update)
(Rel. 40, Last annotation update)
US NUCLEAR RIBONUCLEOPROTEIN H (HNRNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   74
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Gromov P., Madsen P., Gesser B., Tommerup N., Celis J.E.;
RT "Heterogeneous nuclear ribonucleoproteins H, H', and F are members of
RT encoded by expressed subfamily of related but distinct proteins
RT encoded by genes mapping to different chromosomes.";
RL J. Biol. Chem. 270:28780-28789(1995).
RL J. BIOL. Chem. 270:28780-28789(1995).
RL J. RICTIONAL THIS PROTEIN IS A COMPONENT OF THE HETEROGENOUS NUCLEAR
C-!- FUNCTIONAL THIS PROTEIN GAMPLEXES WHICH PROVIDE THE SUBSTRATE
C RIBONUCLEOPROTEIN (HNRNP) COMPLEXES WHICH PROVIDE THE SUBSTRATE
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C FUNCTIONAL, TRANSLATABLE KNNAS IN THE CYTOPLASM. BINDS POLY (RG).
C -!- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOPLASM.
C -!- TISSUE SPECIFICITY: EXPRESSED UBIQUITOSIX.
C -!- SUBCELLULAR LOCATION: EXPRESSED UBIQUITOUSIX.
C -!- SUBCELLULAR LOCATION: RUCLEAR; NUCLEOPLASM.
C -!- TISSUE SPECIFICITY: EXPRESSED UBIQUITON MOTIFS (RRM).
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01-NOV-1997 (Rel. 3
01-OCT-2000 (Rel. 4
HETEROGENEOUS NUCLE
                     This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EW the European Bioinformatics Institute. There are no restruce by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isbsorsend an email to license@isbsbbch).
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P55795;
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Oeltjen J.C., Liu X., Lu J., Malley T.M., Allen R.C.,
Belmont J.W., Gibbs R.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Vorechovsky I., Vetrie D., Holland J., Bentley D.R., Thomas K., Zhou J.N., Notarangelo L.D., Plebani A., Fontan G., Ochs H.D.; "Isolation of cosmid and cDNA clones in the region surrounding the BTK gene at Xq21.3-q22."; Genomics 21:517-524(1994).
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NUCLEAR RIBONUCLEOPROTEIN H' (HNRNP H') (FTP-3).
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RNA-BINDING (RRM) 2.
RNA-BINDING (RRM) 3.
2 X 16 AA GLY-RICH APPROXIMATE REPEATS.
1-1.
1-2.
2 X 19 AA PERFECT REPEATS.
2-1.
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DR Aarhus/Ghent-2DPAGE; 4432; IEF.

DR Aarhus/Ghent-2DPAGE; 4432; IEF.

DR MIM; 601056; ...

DR Pfam; PF00076; rrm; 3.

DR Pfam; PF00076; rrm; 3.

DR PFAM; PF00076; rrm; 3.

DR PROSITE; PS01010; RRM_ENP_1; FALSE_NEG.

PROSITE; PS00030; RRM_ENP_1; FALSE_NEG.

RW Nuclear protein; RNA-binding; Ribonucleoprotein; Repeat.

KW Nuclear protein; RNA-binding; Ribonucleoprotein; Repeat.

FT DOMAIN 111 188 RNA-BINDING (RRM) 1.

FT DOMAIN 289 364 RNA-BINDING (RRM) 2.

FT DOMAIN 234 433 2 X 16 AA GLY-RICH APPROXIMATE REPEATS.

FT REPEAT 374 392 2-1.

FT REPEAT 374 392 2-2.

FT REPEAT 374 372 2-1.

FT REPEAT 374 392 2-2.

SQ SEQUENCE 449 AA; 49263 MW; C892523A638F07C7 CRC64;

DUETY MATCH

DUETY MATCH

BEST Local Similarity 85.7%; Pred. No. 48;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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| 31 | 31 | 31.5 | 32 | 32 | 32 | 32 | 32 | 32 | 32 | 32 | 32 | 32 | 32 | 32 | 32 | 32 | 32 | 32 | 32 | 32 | 32 | 32 | 32 | 32 | 32 |
| 67.4 | 67.4 | 68.5 | 69.6 | 69.6 | 69.6 | 69.6 | 69.6 | 69.6 | 69.6 | 69.6 | 69.6 | 69.6 | 69.6 | 69.6 | 69.6 | 69.6 | 69.6 | 69.6 | 69.6 | 69.6 | 69.6 | 69.6 | 69.6 | 69.6 | 69.6 |
| 146 | 101 | 336 | 1863 | 1845 | 889 | 666 | 657 | 657 | 449 | 449 | 449 | 442 | 415 | 354 | 350 | 346 | 331 | 325 | 325 | 325 | 317 | 301 | 297 | 232 | 154 |
| 14 | 2 | Н | 11 | 14 | 10 | σ | 11 | 4 | 11 | <u>ا</u> | G | 4 | 1, | 10 | | | | 10 | 9 | N | N | N | 4 | 14 | σ |
| Q9J511 | Q9PH51 | Q9HKS5 | Q9JLQ1 | 8ZLW6Ö | Q9FXA5 | Q9VZX5 | Q9R0C5 | Q9UJ28 | P70333 | 035737 | Q23284 | CAMMA T | Q9Z2X1 | Q9SYZ8 | Q9WZ92 | Q9Y4J5 | Q9NPA7 | Q43323 | 064101 | 034558 | Q9L2G1 | 052770 | Q9NP96 | Q9QP22 | Q9MZA9 |
| Q9j511 fowlpox vir | Q9ph51 xylella fas | Q9hks5 thermoplasm | | Q9wjz8 human cytom | Q9fxa5 arabidopsis | Q9vzx5 drosophila | Q9r0c5 rattus norv | Q9uj28 homo sapien | P70333 mus musculu | 7 | | Q9nwy1 homo sapien | Q9z2x1 rattus norv | Q9syz8 arabidopsis | | | Q9npa7 homo sapien | Q43323 saccharum h | | 034558 bacillus su | | | Q9np96 homo sapien | N | Q9mza9 ovis aries |

ALIGNMENTS

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Mallon A.M., Platzer M., Bates R., Gloeckner G., Botcherby M., Nordsiek G., Strivens M.A., Kloschis P., Dangel A., Cunningham D., Straw R., Weston P., Hunter C., Gilbert M., Fernando S., Goodall K., Kerry G., Greystrong J.S., Clark D., Goerdes M., Blechschmidt K., Rump A., Hinzmann B., Mundy C.R., Miller W., Poustka A., Herman G.E., Rhodes M., Denny P., Rosenthal A., Brown S.D.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                              Genome Res. 0:0-0(2000).
EMBL; U82671; AAF44789.1; -.
InterPro; IPR002190; -.
Pfam; PF01454; MAGE; 1.
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ilarity 100.0%;
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Pred. No. 0.32;
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SEQUENCE FROM N.A.

Walker M., Shinn P., Brooks S., Buehler E., Concap A.B., Gonzalez , Kim C., Altafi H., Araujo R., Conn L., Conway A.B., Gonzalez , Kim C., Altafi H., Kremenertskaia I., Lenz C., Li J., Liu Hansen N.F., Huizar L., Kremenertskaia I., Lenz C., Li J., Liu Luros S., Rowley D., Schwartz J., Toriumi M., Vysotskaia V., Lavos S., Rowley D., Schwartz J., Toriumi M., Ecker J.R.; Davis R.W., Federspiel N.A., Theologis A., Ecker J.R.; Davis R.W., Federspiel N.A., Theologis thaliana BAC F23N19 from cl
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01-MAY-2000
01-MAY-2000
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F23N19.5.
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Streptomyces coelicolor.
Streptomyces coelicolor.
Bacteria; Firmicutes; Actinobacteria; Actinobacteria:
Bacteria; Firmicutes; Actinobacteria; Actinobacteria:
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Q9S1R5;
Q1-MAY-2000 (TremBirel. 13,
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Eukaryota; Viridiplantae; Embryophyta; Trachec
Magnoliophyta; endicotyledons; core endicots;
Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                the 8
                                                                                                                                                                                                                                                                                                                                                                                                                           Bentley S. Submitted
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Bentley S.D.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Harris D.;
                                                                                                                                                                                                                                                                 Redenbach M., Kieser H.M., Denapaite Kinashi H., Hopwood D.A.;
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                                                                                                                                                               set of ordered cosmids and a detailed genetic and
8 Mb Streptomyces coelicolor A3(2) chromosome.";
Microbiol. 21:77-961996).
.; AL109972; CAB53266.1; -.
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        Similarity 5; Conserv
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Score 35; UB .
Pred. No. 36;
3; Mismatches
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SEQUENCE FROM N.A.
BLANC COMMUN;
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euasterids II; Asterales;
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66.78;
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01-NOY-1956 (TEMBLrel. 01, Created)
01-NOY-1998 (TEMBLrel. 01, Last sequence update)
01-NOY-1998 (TEMBLrel. 08, Last annotation update)
PROBABLY POSITIONED IN OPERON WITH DOWNSTREAM ORF5.
Plasmid pTA1060.
Bactteria: Fig.
                                                                                                                                                                                                                                     065815; 065814;
01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
07TOCHROME P450 81B1 (EC 1.14.13.53) (TSOFLAVONE 2'
07F081B1 OR CYP81B1C OR CYP81B1S.
Helianthus tuberosus (Jerusalem artichoke).
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Firmicutes; Bacillus/Clostridium Bacillus/Staphylococcus group; Bacillus. NCBI_TaxID=1423;
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eudicotyledons; core eudicots; Asteridae;
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                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                  Query Match
Best Local
Q9VVF8;
Q9VVF8;
01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plasmid pXO2.

Plasmid pXO2.

Bacteria; Firmicutes; Bacillus/Clostridium group; Bactillus/Staphylococcus group; Bacillus.

BCBI_TaxID-1392;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9RMZ0;
01-MAY-2000 (TrEMBLrel.
01-MAY-2000 (TrEMBLrel.
01-MAR-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -i- PATHWAY: INVOLVED IN THE BIOSYNTHESIS OF ISOFLAVONOID-DERIV ANTIMICROBIAL COMPOUNDS OF LEGUMES.
-i- ALTERNATIVE PRODUCTS: TWO FORMS; CYP81B1L (SHOWN HERE) AND CYP81B1S; ARE PRODUCED BY ALTERNATIVE SPLICING.
-i- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
EMBL; AJ000478; CAA04117.; -.
EMBL; AJ000477; CAA04116.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases EMBL; AF188935; AAF13647.1; -. InterPro; IPR001119; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9RMZ0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001128; -. Pfam; PF00067; p450; 1. PRINTS; PR00385; P450.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kumano S., Manter D., Mar
Brown A.E., Jackson P.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. Okinaka R.T., Cloud K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacillus anthracis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PXO2-42.
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                                                                                                                                                                 VKIGNLYVL 475
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                                                                                                                                                                                                                                                                                                                                                                                                              PF00395;
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6; Conserv
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0395; SLH; 3.
                                                                                                                                                                                                                                                                                                                                                   531 AA;
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(TrEMBLrel.
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                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA;
                                                                                                                                                                                                                                                                                                                                                                                      Amidase_3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CYTOCHROME_P450; UNKNOWN_1
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22
40
51
78
78
58914 MW;
                                                                                                                                                                                                                                                                                                                                                   58864 MW;
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85.7%;
                                                                                                                                                                                                                                                                  76.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Martinez Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13,
  13,
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MISSING (IN CYPBIBIS).

MISSING (IN CAA04116).

Y -> S (IN CAA04116).

Y -> Q (IN CAA04116).

P -> Q (IN CAA04116).
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 35; DB
Pred. No. 83;
1; Mismatches
                     Created)
                                                                                                                                                                                                                                               ω,
                                                                                                                                                                                                                                               Score 35; DB
Pred. No. 85;
3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                   9A171DC4ED05CA78 CRC64;
  sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Svensson R.,
                                                               1310 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hill K.K., Keim P., Lamke G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          531
                                                                                                                                                                                                                                                            85;
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                                                                                                                                                                                                                                                                                      2; Length 531;
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RESULT
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DE M
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RA Addams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA George R.A., Lewis S.E., Holt R.A., Evans C.A., Golayne J.D.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Barandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeifer B.D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
RA Hortry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Evangelista C.C., Ferriera S., Pleisolmann W.,
RA Glodek A., Gong F., Gorell J.H., Gu Z., Gubart W.M., Classer K.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Mount S.M., Moyen M. Murphy B., Murphy L., Muzny D., M., Ketchum K.A.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Mosherfi A.,
RA Mount S.M., Melson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Shue B.C., Sidan F., Kanthers R., Deleot M.P., Shen H.,
RA Shue B.C., Sidan F., Kanthers R., Wenter E., Shen H.,
RA Sheng K.-Y., Beatraman D.A., Weinstock G.M., Weissenbach J.,
RA Sheng K.-Y., Beatraman D.A., Weinstock G.M., Weissenbach J.,
RA Sheng X.H., Zhong F.N., Zhong W., Zhang G., Zhan Q.A., Sheng L.,
RA Sheng Y.Y. Ranger G.M., Weinster E., Shen H.,
Ra Spier E. Y., Basarman D.A., Weinstock G.M., Weissenbach J.,
Ra Sheng R., Sheng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                               Q49122
Q49122;
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Eukaryota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-2000 (TrEMBLrel. 13, Last annotation update) CG7692 PROTEIN. CG7692
01-NOV-1996 (TrembLrel. 01, Created)
01-NOV-1996 (TrembLrel. 01, Last sequence update)
01-MAR-2001 (TrembLrel. 16, Last annotation update)
MAU GENE CLUSTER, METHYLAMINE DEHYDROGENASE LARGE AND SMALL SUBUNITS,
AND AMICYANIN, (MAUFBEDACJGLMN) GENES, COMPLETE CDS (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=20196006;
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                                                                                                                                                                                                                                                                                                                                                                 IGHLYLL 225
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                                                                                                                                                                                                  PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         76.1%;
85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             150503 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 35; DB 5;
Pred. No. 2.2e+02;
1; Mismatches (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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RESULT RESULT RESULT IN RESULT IN RESULT RES
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Best Loc
Matches
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O1-MAR-2001 (TIEMBLI
O1-MAR-2001 (TIEMBLI
O1-MAR-2001 (TIEMBLI
3-ISOPROPYLMALTATE I
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J. Bacteriol. 176:4052-4065(1994).
EMBL; L26406; AAB46931.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Methylobacterium group; NCBI_TaxID=408;
006769;
01-JUL-1997 (TremBLrel. 04, Created)
01-JUL-1997 (TremBLrel. 04, Last sequence up
01-JUN-2000 (TremBLrel. 14, Last annotation
HYPOTHETICAL 69.5 KDA PROTEIN.
RV0669C OR MTI376.05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Plasmid.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001387;
Pfam; PF01381; HTH_3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Methylobacterium extorquens.
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9EVH2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Buchnera).";
J. Bacteriol. 183:0-0(2001).
EMBL; AF197453; AAG31393.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LEUB.
                                                                                                                                      006769
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"Vertical Transmission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-UCAL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID-9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Buchnera aphidicola.
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                                                                                                                                                                                                                                                                                          VRIGHLYI 8
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R 139 139
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5; Conserv
                                                                                                                                                                                                                                                                                                                                      Similarity 75.06; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (TremBLrel. 16, Created)
(TremBLrel. 16, Last sequence update)
(TremBLrel. 16, Last annotation update)
MALTATE DEHYDROGENASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                40446 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55
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75
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of Biosynthetic
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                                                                                                                                                                                                                                                                                                                                                          . 9%;
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Rature 393:537-544(1998).
Rature 393:537-544(1998).
Ruberculist; Rv0669c; -.
Ruberculist; Rv0669c; -.
Sp. Fuberculist; Rv0699c; -.
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NCBI_TaxID=1773;
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                       Pfam;
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Eukaryota; Metazoa; Chordata;
Mammmalia; Eutheria; Primates;
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                     PF00024; PAN; 1.
PF00051; kringle;
PF00089; trypsin;
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PROSITE; PS00021; KRINGLE_2; 4
SMART; SM00020; Tryp_SPc; 1.
SMART; SM00020; Tryp_SPc; 1.
Hydrolase; Serine protease.
SEQUENCE 723 AA; 82602 MW;
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01-NOV-1998 (Tremblrel. 0
01-NOV-1998 (Tremblrel. 0
01-MAR-2001 (Tremblrel. 1
T2L5.9 PROTEIN.
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Geisel C., Smith A., Le T.;
"The sequence of A. thaliana T2L5.";
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Magnoliophyta; eudicotyledons; core eudicots;
Brassicales; Brassicaceae; Arabidopsis.
 Q9SIM3
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Pfam; PF00098; zf-CCHC; 1.
Pfam; PF00665; rve; 1.
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C. STRAINE-ZO083487; PubMed=10617197;

X MEDLINE-Z0083487; PubMed=10617197;

A Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,

A Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,

A Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,

A Cronin L.A., Shen M., Vanaken S.E., Umayam L., Tallon L.J., Gill J.E.,

A Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,

A Adams M.D., Freuss D., Nierman W.C., White O., Eisen J.A.,

Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,

A Copenhaver G.P., Fraeser C.M., Venter J.C.;

The Salzberg S.L., Fraeser C.M., Venter J.C.;

The Salzberg S.L., Fraeser C.M., Venter J.C.;

To squence and analysis of chromosome II of Arabidopsis thaliana.";

Nature 402:761-768(1999).

The Mature 402:761-768(1999).

The Mature 402:761-768(1999).
EQUENCE FROM N.A.

CSTRAIN-VC-16 / DSM 4304 / ATCC 49558;

X MEDLINE-98089343; PubMed=9389475;

X MEDLINE-98089343; PubMed=9389475;

X MEDLINE-98089343; PubMed=9389475;

X Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,

A Kletchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,

A Ketchum K.A., Dodson R.J., Gwinn M., Lee N.H., Sutton G.G., Gill S.,

A Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,

Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,

A Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,

A Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,

A Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Hould B.,

A Cotton M.D., Spridgs T., Artiach P., Kaine B.P., Sykes S.M.,

A Overbeek R., Goosyne J.D., Weidman J.F., McDonald L., Utterback T.,

A Overbeek R., Goosyne J.D., Weidman J.F., McDonald S.A.,

A Nason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    028287
028287;
01-JAN-1998
01-JAN-1998
01-MAY-2000
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O1-MAY-2000 (TIEMBLrel. 13, Created)
O1-MAY-2000 (TIEMBLrel. 13, Last sequence update)
O1-MAY-2000 (TIEMBLrel. 16, Last annotation update)
O1-MAR-2001 (TIEMBLREL. 16, Last annotation update)
OUTATIVE RETROELEMENT POL POLYPROTEIN.
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AT2620460.
AT2620470:
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AT26200470:
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SEQUENCE 1
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Interpro; IPR001878; -.
Pfam; PF00098; zf-CCHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=2234;
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SMART; SM00343; ZnF_C2HC; 1.
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1461 AA; 162670 MW;
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(TrEMBLrel. 05, Last sequence update)
(TrEMBLrel. 13, Last sannotation updat)
ING PROTEIN, PUTATIVE.
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Search completed: June 20, Job time: 344 sec
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Best Local Similarity 62.5%;
Matches 5; Conservative
                                                                                                                                                                                                                                                           Query Match 71.7%;
Best Local Similarity 50.0%;
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
PACTOR C PROTEIN PRECURSOR.
Streptomyces griseus.
Bacteria; Filmicutes; Actinobacteria; Actinomycetales; Streptomycineae; Streptomycetales; Streptomycineae; Streptomycetales; NCBI_TaxID=1911;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
EMBL, AF103943; AAC97368.1; -
SIgnal.
SIGNAL 1 38 POTENTIAL.
CHAIN 39 324 FACTOR C TROOTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9Z4K0
Q9Z4K0;
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Biro S., Bekesi I., Vitalis S., Szabo G.;
"A substance effecting differentiation in Streptomyces griseus.
Purification and properties.";
Eur. J. Biochem. 103:359-363(1980).
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PROSTIF; PS00018; EF HAND; UNKNOWN_1.
Hypothetical protein.
SEQUENCE 313 AA; 34574 MW; 4FDD50
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Nature 390:364-370(1997).
EMBL; AE009065; AAB89260.1; ...
TIGR; AF1992; ...
                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Birko Z., Sumegi A., Szeszak F., Vitalis S., Szabo G., Biro S.; "Cloning and sequencing of the factor C gene from Streptomyces griseus 45H.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-45H;
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272 IEIGHVYI 279
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39 324 F
324 AA; 34555 MW;
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                            2001, 14:10:22
                                                                                                                                                                                                                                                              Score 33; DB 2; Length 324
Pred. No. 1.3e+02;
4; Mismatches 0; Indels
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Pred. No. 1.2e+02;
2; Mismatches 1; Indels
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FACTOR C PROTEIN.
; E5F57BA09D2B4EDB CRC64;
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Result
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Maximum DB seq length: 200000000
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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     A_Geneseq_0401:*

1: /SIDS6/gcgdata/geneseq/geneseqp/AA1980.DAT:*

2: /SIDS6/gcgdata/geneseq/geneseqp/AA1981.DAT:*

3: /SIDS6/gcgdata/geneseq/geneseqp/AA1983.DAT:*

4: /SIDS6/gcgdata/geneseq/geneseqp/AA1983.DAT:*

5: /SIDS6/gcgdata/geneseq/geneseqp/AA1985.DAT:*

6: /SIDS6/gcgdata/geneseq/geneseqp/AA1985.DAT:*

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Gapop 10.0 , Gapext 0.5
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Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                            MAGE-21 nonapeptid
MAGE-21 nonapeptid
Immunogenic peptid
MAGE-12/HLA-B44 tu
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                    Hepatocyte growth
Sequence of a pept
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RESULTANT RESULT
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26-MAR-1993;
07-JUN-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic
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ALIGNMENTS

WPI; 1994-100844/12. N-PSDB; Q44753. Boon-falleur T, Van Derbruggen P; (LUDW-) LUDWIG INST CANCER RES MAGE; nonapeptide; cancer; melanoma; breast cancer; HLA; histocompatability; human leucocyte antigen; probe; treatment; MAGE-21 nonapeptide 26-SEP-1994 (first entry) therapy; vaccine. 92US-0938334. 93US-0037230. 93US-0073103. 93WO-US08157 De Plaen E, A Lurquin C, Traversari C;

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RESULT REPUBLICANCE OF THE PROPERTY OF THE PRO
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which bind to a HLA molecule on a cell, and provoke lysis by cytolytic T cells (CTLs) specific for a complex of the HLA molecule and nonapeptide. The nonapeptides can be used diagnostically to identify tumours expressing a particular HLA molecule, or to identify cancer cells. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R99345 standard;
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                                                                                                             R99343-R99350 represent MAGE nonapeptides, based on the tumour rejection antigen region of the full length MAGE sequences. These peptides were used to design the nonapeptides of the invention (see R99337-R99342),
                                                                                                                                                                                                                                                                               New nona:peptide(s) that bind
by specific cytolytic T cells,
tumours and to expand T cells
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Van Den Eynde B,
                                                                                                                                                                                                                                                                                                       to HLA molecule, for diagnosis
                                                                                                                                                                                                                                                                                  in vitro
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iagnosis and
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3.2e+05;
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Van Der E
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Matches 7
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                     Y45390 to Y48214 represent specifically claimed immunogenic peptides having a human major histocompatibility complex (MHC) Class I (also known as human leukocyte antigen (HLA) binding motif. The immunogenic peptides can bind to a specific HLA allele (i.e. HLA-A subtypes HLA-A2.1, A1, A3.2 or A24.1 or HLA-B or C) and induce a cytotoxic T cell response against the antigen from which the peptide is derived. Cytotoxic T lymphocytes (CTLs) which destroy antigen-bearing cells are normally induced by an antigen in the form of a peptide fragment bound to a HLA molecule, rather than the intact foreign antigen itself, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA; immune response; T cell activation; major histocompatibility complex; cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;
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             are particularly important in tumour rejection and in fighting viral
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100.0%;
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3.2e+05;
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The peptides are therefore useful therapeutically

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      This peptide is a tumour rejection antigen presented by a HLA-B44 molecule and derived from a MACE-12 tumour rejection antigen precursor (TRAP). Claimed tumour rejection antigens (W23038-4) are able to bind to HLA-B44 positive cells, making them useful in identifying cells which present HLA-B44 molecules on their surfaces for use in the diagnosis and therapy of cellular abnormalities. The complex of the tumour rejection antigen and HLA molecule provokes a cytolytic T cell response. The tumour rejection antigens, or complexes of tumour rejection antigens and HLA-B44, can be used as vaccines to treat disorders characterised by expression of the TRAP molecule such as cancer, especially melanoma. Vaccines can also be prepared from cells which present the tumour rejection antigens and several from cells which present the tumour rejection antigens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or prevent viral infections and cancers in mammals (especially humans) e.g. prostate cancer, hepatitis B and C, AIDS, and renal carcinoma. They can be administered as vaccines to elicit an immune response in individuals susceptible or otherwise at risk of viral infection or cancer, or used to treat chronic or acute conditions. They are also useful diagnostically, and can be used to induce a cytotoxic T cell response, by contacting a cytotoxic T cell with the peptide e.g. to produce CTLs ex vivo for infusion back into a partient. The polynuclectides encoding the immunogenic peptides are also useful therapeutically and for immunisation as above.
                                                                                                                                                                                                                                                     Tumour rejection antigens presented by molecules - useful to identify HLA-B44 and therapy of cellular abnormalities
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| vrighly 9
tumour rejection antigen/HLA complexes on
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tumour rejection antigen
                                                                                                                                                                                                                                                                                                                                                                       Coulie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     82.6%;
                                                                                                                                                                                                                                                                                                                                                                       ָש
                                                                                                                                                                                                                         English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                       Herman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 38;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                       'n
                                                                                                                                                                                                                                                                      human leukocyte antigen B44 positive cells for diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               T lymphocyte; cancer;
                                                                                                                                                                                                                                                                                                                                                                       Luescher
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 BB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20;
their surface,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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RESULT
Y05902
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8 X C C
                                     The present sequence represents in-chain hydroxylase CYP81B1 of Jerusalem artichoke. CYP81B1 is a microsomal cytochrome P450 that catalyses the omega-2, omega-3 and omega-4 hydroxylation of capric, lauric and myristic acids. The major metabolite is the comega-3-hydroxylated compound. The invention provides isolated nucleic acids (see x58400-06) encoding plant fatty acid hydroxylases (see v05896-902). Also claimed are host cells, transgenic plants and compositions consisting of the plant fatty acid hydroxylase, a process for isolating additional fatty acid hydroxylase genes from a plant, and a process of altering the fatty acid composition in a plant by expressing the plant fatty acid hydroxylase in a transgenic plant. Manipulating or epoxidating a fatty acid composition in a plant by expressing the plant fatty acid acid composition in a plant by expressing the plant fatty acid acid composition in a plant by expressing the plant fatty acid acid composition in a plant by expressing the plant fatty acid acid composition in a plant by expressing the plant fatty acid acid composition in a plant by expressing the plant fatty acid acid content of plants will modify resistance to drought and cattack by insects and other pests. The transgenic plants may also be used as sources of hydroxylated and epoxidized fatty acids useful in the manufacture of e.g. lubricants, anti-slip agents,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local S
Matches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                            Batard Y, Benveni
Helvig C, Le Boug
Werck-Reichhart D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Helianthus tuberosus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              In-chain hydroxylase; transgenic plant; lipid; hydroxylation; oliseed; vegetable oll; crop protection; Jerusalem artichoke; CYP81B1; cytochrome P450.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           as non-proliferative transfectants.
Sequence
                              plasticisers, coating
                                                                                                                                                                                                                                                                                                                                 Example
                                                                                                                                                                                                                                                                                                                                                              Nucleic acid encoding plant fatty acid hydroxylases
                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1999-264030/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9918224-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Jerusalem artichoke in-chain hydroxylase CYP81B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Y05902;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05902 standard; Protein; 505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 VRIGHLY 7
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                                                                                                                                                                                                                                                                                                                                 4;
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                                                                                                                                                                                                                                                                                                                                 Fig 20A-B; 157pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10
505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Benveniste
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Le Bouquin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cancer cells and non-proliferative
                            agents, detergents and surfactants
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Pinot F, Salaun
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Pred. No
                                                                                                                                                                                                                                                                                                                              English.
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0.099;
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Tijet
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RESULT
R25692
ID %2
XX
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Best Local Similarity
"hehes 7; Conserv?
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Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                              Y34584-Y35879 represent the proteins encoded by all the open reading frames in the complete genome (see X91990) of Chlamydia pneumoniae. C. pneumoniae causes respiratory disease such as pneumonia and bronchitis and is thought to be a contributing factor in heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema nodosum or pharyngitis. The polypeptides encoded by the open reading frames of the C. pneumoniae genome (see Y34584-Y35879) can be used in immunogenic compositions as vaccines. Vectors containing C. pneumoniae nucleotides sequences can also be used as immunogenic compositions, especially where the vector directs the expression of a neutralising epitope of C. pneumoniae.
                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                   Genome sequence of Chlamydia pneumoniae
                                                                                                                                                                                                                                                                                                                                                                               Griffais
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W09927105-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chlamydia pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis; sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine; neutralising epitope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Y34971;
          N25692 standard; Protein; 189
                                                                                                                                                                                                                                                                                                                                                                                                                         04-NOV-1998;
21-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Y34971 standard; Protein; 621
                                                                                                                                                                                                                                                                                                                                                                                                    (GEST ) GENSET
                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Amino acid sequence of a Chlamydia pneumoniae protein
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||||||||
| 40 ighlyll 46
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                                                                                   1 VRIGHLYI 8
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                                                                                                                                                                                                                                                                                                                                                          1999-357842/30
                                                                                                                                                                                                                                                                                                              885-886; Disclosure; 1912pp; English.
                                                               vrignlyi 33
                                                                                                                                                                                                                                                                                                                                                                               R
                                                                                                                                                             621
                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                             AA;
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97FR-0014673.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         98WO-IB01890
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85.7%;
                                                                                                                  76.1%;
87.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Mismatches
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                                                                                                                   Score 35; DB Pred. No. 38;
           AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA.
                                                                                                         Mismatches
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                                                                                                                            20;
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                                                                                                                            Length 621;
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                                                                                                         Indels
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                                                                                                         0;
                                                                                                                                                                                                                 pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0,
                                                                                                         Gaps
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                                                                                                         0;
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RESULT
Y98485
                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 5
                   Transporter system; nucleic acid delivery; carcinogenesis; cardiovascular disease; in:
                                                                    31-JUL-2000
                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                        See also R25676-92,
                                                                                                                                                                                                                                                                                This sequence is made up of exons XV growth factor.
                                                                                                                                                                                                                                                                                                               Disclosure; Page 22; 28pp; Japanese.
                                                                                                                                                                                                                                                                                                                                  Recombinant human hepatocyte growth factor and DNA encoding it useful for diagnosis and treatment of hepatic disease and transgenic animal prepn.
                                                                                                                                                                                                                                                                                                                                                                          WPI; 1992-265591/32.
N-PSDB; Q26727.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HGF; enhance growth; preparing transgenic animals; hepatic disease;
clinical diagnostic reagent; drug.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Exons XV to XVIII of human hepatocyte growth factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R25692;
Synthetic
                                                Hepatocyte growth factor Pep 20 used in nucleic acid transporter system.
                                                                                        Y98485;
                                                                                                             Y98485 standard; Protein; 697
                                                                                                                                                                                                                                                                                                                                                                                                                                      19-NOV-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          19-NOV-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-JUN-1992.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-JAN-1993
                                                                                                                                                                                                                                                                                                                                                                                                      (NAKA/) NAKAMURA T.
(TOYM ) TOYOBO KK.
                                                                                                                                                            90
                                                                                                                                                                                1 VRIGHLYIL 9
                                                                                                                               8
                                                                                                                                                           :|: ||||:
| lrvahlyim
                                                                                                                                                                                                   Similarity
5; Conserv
                                                                                                                                                                                                                                                    189 AA;
                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                    (first entry)
                                                                                                                                                              98
                                                                                                                                                                                                                                                                                                                                                                                                                                      90JP-0314548
                                                                                                                                                                                                                                                                                                                                                                                                                                                          90JP-0314548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= exon XVII
132..187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= exon XVI
83..131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label= exon
48..82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
1..47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label= exon XVIII
                                                                                                                                                                                                                                                                         Q26713-27
                                                                                                                                                                                                             73.9%;
                                                                                                                                                                                                   Score 34; DB
Pred. No. 17;
3; Mismatches
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                                                                                                             B
                                                                                                                                                                                                                                                                                            to
                     infection
                                                                                                                                                                                                                                                                                             XVIII of
                            gene therapy;
                                                                                                                                                                                                                       13;
                                                                                                                                                                                                   1
                                                                                                                                                                                                                       Length 189;
                                                                                                                                                                                                                                                                                            human hepatocyte
                                                                                                                                                                                                     Indels
                              cancer;
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0;

US6033884 - A.

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RESULT
Y5900 ID Y590
ID Y590
ID Y590
XX Y59
AC Y59

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to a transporter system for delivering CC nucleic acid to a cell. The system comprises a nucleic acid binding CC complex, consisting of a binding molecule bonded non-covalently to the CC mucleic acid, and covalently to a surface ligand, and a lytic agent. The CC binding molecule is spermine or a spermidine derivative. Nucleotide Sequences A3663-A3652 and peptide sequences Y94850 are used in the construction of the transporter system of the invention. The CC transporter system is used in gene therapy, particularly to deliver CC uncleic acids to hepatocytes, muscle cells or bone forming cells, e.g for CC treating cardiovascular disease, cancer, and infection. The transporter CC systems are also used to create transgenic animals (as models for human CC arcinogenesis or disease or for drug testing). Other uses include CC transforming cells to produce proteins, or transferting cells in vitro CC to study the function of the nucleic acid. The use of a surface ligand CC allows specific targeting of selected cells and tissues. The lytic agent provides for release of the nucleic acid into the cellular interior, from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local S
Matches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                System for transporting nucleic acid into cells, useful e.g. in g
therapy and for generating transgenic animals, comprises binding
linked to nucleic acid, surface ligand and lytic agent -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-281993/24.
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19-MAR-1993;
      14-DEC-1993;
                                                                                                                                                                                                                                           Synthetic
                                                                                                                                                                                                                                                                                                                                                            Nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence of a peptide ligand Pep20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-MAR-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     endosomes, without requiring endosomal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (BAYU ) BAYLOR COLLEGE MEDICINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-DEC-1993;
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                                                                                                                       30-NOV-1999
                                                                                                                                                                                                                                                                                                     nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Y59030 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                            acid transport system; NTS; cell surface receptor; cytosis;
membrane; lysis moiety; transgenic animal; human disease;
acid delivery; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity 55.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              697 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sparrow J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92US-0855389
93WO-US02725
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      93US-0167641
                                                                95US-0460890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 peptide; 697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    73.98;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 34;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       core 34; DB red. No. 70; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or lysosomal degradation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Woo SLC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 697;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Smith LC
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ding agent
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Query Match
Best Local Similarity
"~+~hes 5; Conserv
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B45838
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a nucleic acid transport system (NTS) for Cd delivering nucleic acid into a cell. The NTS contains but is not limited Ct to 5 components: (a) the nucleic acid or a macromolecule to be delivered; CC (b) a molety that recognizes and binds to a cell surface receptor or C antigen or is capable of entering a cell through cytosis; (c) a nucleic acid or macromolecular molecule binding molety; (d) a molety that is CC capable of moving or initiating movement through a nuclear membrane; and/CC or (e) a lysis molety that enables the transport of the entire complex CC from the cell surface directly into the cytoplasm of the cell. The NTS CC delivers nucleic acid into the cellular interior as well as the nucleus CC of specific cells. The NTS can be used to treat disorders by targeting specific animals for assessing human disease, such as cancer, in an animal model. The NTS can be used in vitro with tissue culture cells which allows the role of various nucleic acids to be studied by targeting specific expression into specifically targeted tissue culture cells. The CC systs agent within the NTS avoids the problem of endosomal/lysosomal
            14-DEC-1993;
20-MAR-1992;
19-MAR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-MAR-1992;
19-MAR-1993;
14-DEC-1993;
                                                                                                                                         US6150168-A.
                                                                                                                                                                                                                   Nucleic acid delivery; nucleic acid transporter system; hormone; enzyme; growth factor; clotting factor; apolipoprotein; receptor; drug; oncogene; tumor antigen; tumor suppressor; viral antigen; parasitic antigen;
                                                                                                                                                                                                                                                                                                                                                    B45838;
                                                                                                                                                                                                                                                                                                                                                                                 B45838 standard; Protein; 697 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Fig 23A; 107pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acid transport system, useful for creating transgenic animals for assessing human disease such as cancer in an animal model -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-038262/03
                                                                           05-JUN-1995;
                                                                                                                                                                         Unidentified
                                                                                                                                                                                                      bacterial antigen.
                                                                                                                                                                                                                                                                                                                    21-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (BAYU ) BAYLOR COLLEGE MEDICINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                              :|: |||:
598 lrvahlyim 606
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                                                                                                                                                                                                                                                                                     acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                   transporter system peptide ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92US-0855389.
93WO-US02725.
93US-0167641.
             93US-0167641.
92US-0855389.
93WO-US02725.
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                                                                           9508-0460971
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 34; DB
Pred. No. 70;
3; Mismatches
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                                                                                                                                                                                                                                                                                     SEQ
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This invention describes a novel system (I) for delivering a nucleic acid CC to a cell, comprising a binding complex comprising a ligand binding CC molecule noncovalently bound to a nucleic acid and covalently linked to a CC surface ligand, and a second binding complex comprising a second binding CC molecule noncovalently bound to a nucleic acid and covalently linked to a covalent ligand. The complexes are simultaneously bound to the nucleic CC acid. The nucleic acid transporter system can also be used in a method CC for the in vivo targeting of the insertion of DNA into a cell. It can CC also be used in processes for producing transformed cell lines. The CC system can be used to deliver a variety or proteins and polypeptides, CC such as hormones, growth factors, enzymes, clotting factors, tumor complexesors, viral antigens, drugs, oncogenes, tumor antigens, tumor acceptors wirely system uses lysis agents to overcome the problems of CC endosomal/lysosomal degradation seen with prior art systems.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acid transporter system for delivering nucleic acid into a cell, useful for delivering proteins and polypeptides to cells, including growth factors, enzymes, hormones, and tumor suppressors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI;
             P-PSDB; R07144.
                                                 Higashio K; Mistuda S;
                                                                                                  16-JAN-1990;
03-OCT-1989;
                                                                                                                                      03-SEP-1990;
                                                                                                                                                                                      W09010651-A
                                                                                                                                                                                                            Peptide
                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                        TCF II;
                                                                                                                                                                                                                                                                                                Tumour
                                                                                                                                                                                                                                                                                                                       31-JAN-1991
                                                                                                                                                                                                                                                                                                                                               R07144;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gottchalk S,
                          WPI; 1990-304990/40
                                                                         (SNOW)
                                                                                                                                                              20-SEP-1990
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| lrvahlyim 606
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5; Conser
                                                                          SNOW
                                                                                                                                                                                                                                                                       glycoprotein; fibroblasts; anticancer agent
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                                                                          BRAND MILK PRODUCTS
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                                                                                                  90JP-0006692.
                                                                                                                                      90WO-J000314
                                                                                                                                                                                                            Location/Qualifiers 1...29
                                                                                                                                                                                                                                                                                                                                                                     protein; 723
                                                                                                                                                                                                                                                                                                factor II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           73.9%;
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                                                 Shima N; Itagaki Y; Nagao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cristiano
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 34; DB
Pred. No. 70;
3; Mismatches
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R14307
ID R14307
  Дb
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Best Local
 New plasminogen-like growth factor protein - having mitogenic activity on melanocytes, epithelial cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R14307;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                          Rubin
                                                                                                                                                                                                                                                                                                          Peptide
                                                                                                                                                                                                                                                                                                                                              Peptide
                                                                                                                                                                                                                                                                                                                                                            Key
                                                                          JS,
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from a cDNA library prepd. from RNA extd. from fibroblast IMR-90 cells (ATCC CCL-186). The N-terminal of the alpha chain is unclear. The sequence shows homology to bHGF except between AAS 162 and 166 of this sequence which is absent from the TCF-II sequence. The DNA can be used to produce the TCF-II by recombinant pank trophology.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA technology. TCF II is an anticancer agent and induces differentiation of leukaemia cells, enhances cell-mediated immunity, and accelerates the proliferation of human blood vessel endothelial cells and hepatic parenchymal cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human glycoprotein having antitumour activity - for inducing differentiation of leukaemia cells and enhancing cell mediated
WPI; 1991-317957/43.
N-PSDB; Q14182.
                                                                                                                                                                                                                                                                                                                       Cleavage-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mitogenic activity; PLGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plasminogen-like growth factor protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-JAN-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Fig 15; 73pp;
                                                                                    (USSH ) NAT INST OF HEALTH
                                                                                                                       14-SEP-1990;
                                                                                                                                                      14-SEP-1990;
                                                                                                                                                                                        17-SEP-1991.
                                                                                                                                                                                                                          US7582063-A
                                                                                                                                                                                                                                                                        Active-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
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624 lrvahlyim 632
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence was deduced from the cDNA obtd. from a clone isolated m a cDNA library prepd. from RNA extd. from fibroblast IMR-90
                                                     Chan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        723 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                       90US-0582063
                                                                                                                                                       90US-0582063
                                                     AML,
                                                                                                                                                                                                                                                                        /note= "conserved, relative to plasminogen"
529
                                                                                                                                                                                                                                                                                                                        /*tag= b
/note= "mature peptide"
489..490
                                                                                                                                                                                                                                                                                                                                                                          /note= "signal peptide"
33..723
                                                                                                                                                                                                                                                                                                                                                                                                     /*tag=
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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                                                     Aaronson
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Pred. No.
                                                     SA;
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73;
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RESULT RE
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Best Local
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The sequence was deduced from a portion of HLC3, one of two clones, (for HLC2 see R15623) isolated from a cDNA library prepd. from mRNA extracted from human leukocytes. HLC2 has almost the same sequence as HLC3 except for five residues (162-166) in HLC2 which do not appear in HLC3. HLC3 shows similar characteristics to the human liver-derived HGF identified in Nature, 342, 440, 1989, but differs at 14 positions in the amino acid sequence. The DNA sequence can be expressed and the resulting protein, recombinant HGF, used in hepatocyte research, esp. into the mechanism of hepatoma, and to prepare anti-HGF antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure;
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                                                                                                                                                                                                                                                                                                                                                    Recombinant human leukocyte-derived hepatocyte growth factor with DNA encoding it, recombinant expression vectors and transformant cells expressing it.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-JUN-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human leukocyte-derived HGF encoded by clone HLC3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-MAR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R15624;
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                                                                                                                                                                                                                                                                                                   Claim 3; Fig 3; 33pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nakamura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ( MYOT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-JUN-1990;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hepatocyte growth
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Tsuda E;
                                                                                                          A human foetal lung fibroblast library was screened with a synthetic probe coding for the N-terminal sequence of TCF-II. A cDNA clone was isolated and sequenced. The coding sequence can be incorporated into a plasmid and transformed into a microorganism for production of TCF-II. The protein itself can be used as a liver cell growth factor or a tumour cell killing factor. See also Q21067-9.
                                                                                                                                                                                 Claim 6; Fig 1; 47pp; Japanese.
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N-PSDB; Q21066.
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See also R25676-92, Q26713-27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Recombinant human hepatocyte growth factor and DNA encoding it useful for diagnosis and treatment of hepatic disease and transgenic animal prepn.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (NAKA/) NAKAMURA T. (TOYM ) TOYOBO KK.
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CC emBL; L18877; AAA19023.1; -.

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DR Pfam; PF01454; MAGE; 1.

FT CONFLICT 10 10 10 C-> S (IN REF. 2).

FT CONFLICT 10 300 300 P-> S (IN REF. 2).

FT CONFLICT 300 300 P-> S (IN REF. 2).

SO SEQUENCE 314 AA; 34802 MW; 3F0787CECD8816A5 CRC64;

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(CDP-DAG

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MAGNINA MAGNIN
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P43356;
01-NOV-1995
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HUMAN
                                                                                                                                                                                                MUTAGEN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      autologous cytolytic T lymphocytes.";

J. EXP. Med. 179;921-930(1994).

-i- FUNCTION: NOT KNOWN, THOUGH MAY PLAY A ROLE IN EMBRYONAL

-i- FUNCTION: NOT KNOWN, THOUGH MAY PLAY A ROLE IN EMBRYONAL

DEVELOPMENT AND TUMOR TRANSFORMATION OR ASPECTS OF TUMOR

PROGRESSION. ANTIGEN RECOGNIZED ON A MELANOMA BY AUTOLOGOUS

CYTOLYTIC T LYMPHOCYTES.

-i- TISSUE SPECIFICITY: EXPRESSED IN MANY TUMORS OF SEVERAL TYPES,

-i- TISSUE SPECIFICITY: EXPRESSED IN MANY TUMORS OF SEVERAL TYPES.
                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the E the European Bioinformatics Institute. There are no rest use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entities requires a license agreement (See http://www.isb-or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaugler B., van den Eynde B., van der Bruggen P., 1
Gaforio J.J., de Plaen E., Lethe B., Brasseur F., I
"Human gene MAGE-3 codes for an antigen recognized
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
MELANOMA-ASSOCIATED ANTIGEN 2 (MAGE-2 ANTIGEN).
                                                                                                                                                                                                                                                                                                Pfam; PF01454; MAGE;
                                                                                                                                                                                                                                                                                                                                                                        EMBL; L18920; AAA17729.1;
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MEDLINE=94102805; PubMed=8276455;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WITH MAGE-12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VVRIGHLYIL 10
                          VVRIGHLYIL 10
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rota; Metazoa; Chordata;
ia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10;
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                                                                        Similarity
8; Conserv
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                                                                                                                                                                                                                                                                        Multigene family; Tumor antigen.
                                                                                                                                                                                                                                                                                                                     IPR002190;
                                                                                                                                                                                                  314 · AA;
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                                                                        Conservative
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                                                                     Pred. No. 4;
0; Mismatches
                                                                                             Score 37;
Pred. No.
                                                                                                                                                                                                POLY-SER.
V->D: IMPROVES ABILITY TO BIND; 844F16335A2BECE7 CRC64;
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Catarrhini;
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Boon T.;
d on a melar
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004928; 048808;
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
PHOSPHATIDATE CYTIDYLLTIANSFERASE (EC 2.7.7.41) (CDP-DIG
SYNTHASE) (CDP-DIGLYCERIDE PYROPHOSPHORYLASE) (CDP-DIAC
SYNTHASE) (CDS) (CTP-PHOSPHATIDATE CYTIDYLLTIANSFERASE)
                                                                                                                        TRANSMEM
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cheuk R., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson Rhan S., Kim C., Altafi H., Bei B., Chin C., Chiou J., Choi E., Conn L., Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsky N., Ryuyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Theologis A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N. Theologis A., Ecker J.;
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.

-I- PUNCTION: MAY BE INVOLVED IN THE SYNTHESIS OF MINOR PHOSPHOLIPII AND IN MODULATION OF IP3-MEDIATED SIGNAL TRANSDUCTION.

-I- CATALYTIC ACTIVITY: CTP + PHOSPHATIDATE - PYROPHOSPHATE +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                   rram; PFU1148; Cytidylyltrans; PROSITE; PS01315; CDS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X94306; CAA63969.1; EMBL; AC003113; AAF70845.1
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STRAIN-GV. C24; TISSUE-Flower, and Siliquencine-97239925; PubMed=9085581;
Kopka J., Ludewig M., Mueller-Roeber B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Embryophyta;
Magnoliophyta; eudicotyledons; core eud
Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Complementary DNAs encoding eukaryotic-type cytidine-5'-diphosphate-diacylglycerol synthases of two plant species."; Plant Physiol. 113:997-1002(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana (Mouse-ear cress).
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                                                                                                                                                                                                                                                                           Transmembrane.
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SUBCELLULAR LOCATION: INTEGRAL MEMBRAN
SIMILARITY: BELONGS TO THE CDS FAMILY.
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Similarity 7; Conserv
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149
206
246
321
421
  Conservative
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226
241
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dicots; Rosidae; eurosids II;
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EMBL; AE002200; J
EMBL; AP002546; J
TIGR; CP0383; -.
                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-20330349; PubMed-10871362; Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K., Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.; "Comparison of whole genome sequences of Chlamydia pneumoniae J138 "Compara and CWL029 from USA."; Nucleic Acids Res. 28:2311-2314(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg White O., Hickey E.K., Peterson J., Utterback T., Berry Linher K., Weidman J., Khouri H., Craven B., Bowman C., Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Eisen J., Fraser C.M.; "Genome sequences of Chlamydia trachomatis MoPn and Chlapneumoniae AR39.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=99206606; PubMed=10192388; Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W., Olinger L., Grimwood J., Davis R.W., Stephens R.S.; "Comparative genomes of Chlamydia pneumoniae and C. trachomatis."; Mat. Genet. 21:385-389(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chlamydia pneumoniae (Chlamydophila pn. Bacteria; Chlamydiales; Chlamydiaceae; NCBI_TaxID=83558;
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Q9Z8H0; Q9ZQ95;
Q1-CCT-2000 (Rel. 40, Created)
01-CCT-2000 (Rel. 40, Last sequence update)
01-CCT-2000 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-CWL029;
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18
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|| :||||
6 VVYMGHLYI 74
VRIGNLYI
                                                    VRIGHLYI 9
                                                                                                           Similarity 7; Conser
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25
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                                                                                                                                                                                                                                                      68308
                                                                                                                                    70.0%;
                                                                                                                                                                                                                                                      M₩;
                                                                                                        Score 35; DB
Pred. No. 20;
1; Mismatches
                                                                                                                                                                                                                                                      40B1F831E02DC6D4 CRC64;
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ae; Chlamydophila
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20;
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                                                                                                           0
                                                                                                                                                                Length 613;
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y K., Bass S.,
, Dodson R.,
, Salzberg S.L.,
                                                                                                        0;
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RESULT 6
HGF_HUMAN
ID_HGF_HUMAN
AC P14210;
DT 01-JAN-1990 (
DT 01-AUG-1991 (
DT 01-CUG-2000 (
DE HEPATOCYTE GR
     DE DIT DAC
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RY "Mutations in Bartonella bacilliformis gyrB confer resistance to recommermycin Al.";

RT coummermycin Al.";

RT Antimicrob. Agents Chemother. 42:2906-2913(1998).

RL Antimicrob. Agents Chemother. 42:2906-2913(1998).

C. :FUNCTION: DNA GYRASE NEGATIVELY SUPERCOILS CLOSED CIRCULAR DOUBLE-CIRCULAR DOUBLE-CIRCULAR DOUBLE-STRANDED DNA IN AN ATP-DEPENDENT MANNER AND ALSO CATALYZES THE INTERCONVERSION OF OTHER TOPOLOGICAL ISOMERS OF DOUBLE-STRANDED CONTROL ISOMERS OF DOUBLE-STRANDED DNA RINGS, INCLUDING CATENANES AND KNOTTED RINGS.

C. -- CATALYTIC ACTIVITY: ATP-DEPENDENT BREAKAGE, PASSAGE AND REJOINING OF DOUBLE-STRANDED DNA.

C. -- SUBUNIT: MADE UP OF TWO CHAINS. THE A CHAIN IS RESPONSIBLE FOR DNA BREAKAGE AND REJOINING; THE B CHAIN CATALYZES ATP HYDROLYSIS. THE ENGYME FORMS AN A2B2 TETRAMER.

C. -- SIMILABITY: BELONGS TO TYPE II TOPOISOMERASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
Matches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR002288; ...

Pfam; PF00204; DNA_COPOISOII; 1.

Pfam; PF00204; DNA_COPOISOII; 1.

PRINTS; PR00418; TPI2FAMILY.

PROSITE; PS00177; TOPOISOMERASE_II; 1.

PROSITE; PS00177; TOPOISOMERASE_II; 1.

TOPOISOMERASE; Isomerase; ATP-binding; An VARIANT 124 124 G -> S (IN C VARIANT 184 184 R -> Q (IN C VARIANT 214 214 T -> A (IN C VA
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P94281;
P94281;
15-DEC-1998
15-DEC-1998
01-OCT-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Battisti T
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Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Bartonellaceae; Bartonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GYRB
01-JAN-1990 (Rel. 13, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation updat
HEPATOCYTE GROWTH FACTOR PRECURSOR (SCATTER
(HEPATOPOEITIN A).
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                                                                                                                                                                                                                                                                                                575 LIRAGHLYL
                                                                                                                                                                                                                                                                                                                             1 VVRIGHLYI
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                                                                                                                                                                                                                                                                                                                                                                                                      Similarity 55. 5; Conservative
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(Rel. 37, Last sequence up
(Rel. 40, Last annotation
SUBUNIT B (EC 5.99.1.3).
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                                                                                                                                                                STANDARD;
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G -> S (IN COUMERNYCIN AL MUTANT).

R -> Q (IN COUMERNYCIN AL MUTANT).

T -> A (IN COUMERNYCIN AL MUTANT).

T -> I (IN COUMERNYCIN AL MUTANT).

T -> I (IN COUMERNYCIN AL MUTANT).
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; Pred. No. 23;
3; Mismatches
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                             FACTOR)
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MEDLINE=91207365; PubMe
Yoshiyama Y., Arakakai
Nakayama H., Gohda E.,
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TISSUE-Embryonic fibroblast;
MEDLINE-91334393; PubMed-1831266;
MEDLINE-9134494; N., Hartmann G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature
[5]
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"Isolation and expression of cDAh for different forms
growth factor from human leukocyte.";
Biochem. Biophys. Res. Commun. 172:321-327(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seki T., Ihara I., Sugimura A., Shimonishi M., Nishizawa Asami O., Hagiya M., Nakamura T., Shimizu S.:
"Isolation and expression of or..."
| Irowth factor | I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       growth factor."
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HOMO Sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
MCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CARBOHYDRATE-LINKAGE SITE 476.
MEDLINE=93129192; PubMed=1482348;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nakamura T., Nishizawa T., Hagiya M., Seki T., Shimoni
Sugimura A., Tashiro K., Shimizu S.;
"Molecular cloning and expression of human hepatocyte
Nature 342:440-443(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=89392017; PubMed=2528952; Miyazawa K., Tsubouchi H., Naka D., Arakaki N., Nakayama H., Hirono S., Coba C., Coba 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE-91340155; Seki T., Hagiya M.
                           Lokker N.A., Mark M.R., Luis E.A., Bennett G.L., Robbins Haker J.B., Godowski P.J.;
Baker J.B., Godowski P.J.;
"Structure-function analysis of hepatocyte growth factor:
identification of variants that lack mitogenic activity yo
                                                                                                                                                                                                                                                                                                                                                                                                                                                Shimizu N., Hara H., Sogabe T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Weidner K.M., Arakaki N., Hartmann G.
Rieder H., Fonatsch C., Tsubouchi H.,
                                                                                                                                                                                                                                                                                                                                                                            "Hepatocyte growth factor is linked on the alpha chain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hepatocyte growth
Proc. Natl. Acad.
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Seki T., Hagiya M., Shimonishi M.,
"Organization of the human hepatoc;
Gene 102:213-219(1991).
                                                                                                                                                                                                        MEDLINE=92331602;
                                                                                                                                                                                                                                                     MUTAGENESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Evidence for the identity
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affinity
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Gohda E., Kitamura N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pubmed=1826837;
                                                                                                                                                               PubMed=1321034;
M.R., Luis E.A.,
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Sci. U.S.A.
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Pfam; PF00024; PAN; 1.
Pfam; PF00051; Kringle; 4.
Pfam; PF00089; trypsin; 1.

PRINTS; PRO0018; KRINGLE.
PRINTS; PRO0722; CHYMOTRYPSIN.
PROSTTE; PS00021; KRINGLE_1; 4
PROSITE; PS50070; KRINGLE_2; 4

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Ultsch M., Lokker N.A., Godowski P.J.,
"Crystal structure of the NKI fragment
factor at 2.0-A resolution.",
Structure 6:1383-1393(1998).
-i- FUNCTION: HGF re a resolution."
                                                                                                                                                                      GlycoSuiteDB;
MIM; 142409;
                                                                                                                                                                                                                                                                                                                                                                                 the European Bioinformatics Institute. There are no rest use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entities requires a license agreement (See http://www.isbor send an email to license@isb-sib.ch).
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Zhou H., Mazzulla M.J., Kaufman J.D., Stahl S.J., Wi
Rubin J.S., Bottaro D.P., Byrd R.A.;
"The solution structure of the N-terminal domain of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRUCTURE
                                                                                                                         MEROPS; S01.976;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: HGF IS À POTENT MITOGEN FOR MATURE PARENCHYMAL HEPATOCYTE CELLS, SEEMS TO BE AN HEPATOTROPHIC FACTOR, AND AS GROWTH FACTOR FOR A BROAD SPECTRUM OF TISSUES AND CELL IT HAS NO DETECTABLE PROTEASE ACTIVITY.
SUBUNIT: DIMER OF AN ALPHA CHAIN AND A BETA CHAIN LINKED B DISULFIDE BOND.
SIMILARITY: CONTAINS 4 KRINGLE REGIONS.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS
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                                                                                                      142409; -
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SEQUENCE FROM N.A., AND SEQUENCE OF 490-504.

TISSUB-Mammary fibroblast;

MEDLING-94183257; PubMed-8135822;

Sasaki M., Nishio M., Sasaki T., Enami J.;

Gentification of mouse mammary fibroblast-derived

"Identification of arouth factor.";
                                                                                                                                                                                                                                                       HGF_MOUSE STANDARD; PRT; 708048; 064007; 061662; 01-NOV-1995 (Rel. 32, Created) 01-NOV-1995 (Rel. 32, Last sequence up 01-OCT-2000 (Rel. 40, Last annotation HEPATOCYTE GROWTH FACTOR PRECURSOR (SC
                                                                                                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10090;
 SEQUENCE FROM N.A. TISSUE-Liver;
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Biophys. Res. Commun. 199:
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 MGD; MGI:96079; Hgf.
InterPro; IPR000001; -.
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InterPro; IPR001314; -.
Pfam; PF00024; PAN; 1.
Pfam; PF00051; kringle; 4.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00018; KRINGLE.
PRINTS; PR000722; CHYMOTRYPSIN.
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EMBL; D10213; BAA01065.1; -
EMBL; S71816; AAB31855.1: -
EMBL; S72307; CAA51054.1; A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hepatocyte growth factor.";
Biochim. Biophys. Acta 1216:299-303(1993).

-I- FUNTCTION: HGF IS A POTENT MITOGEN FOR MATURE PARENCHYMAL
-I- FUNTCYTE CELLS, SEEMS TO BE AN HEPATOTROPHIC FACTOR, AND ACTS
AS GROWTH FACTOR FOR A BROAD SPECTRUM OF TISSUES AND CELL TYPES.
IT HAS NO DETECTABLE PROTEASE ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=94363381; PubMed=8081873;
Lee C.C., Kozak C.A., Yamada K.M.;
"Structure, genetic mapping, and expression of
factor gene.";
                                                                                                                                                                                                                                                            CHAIN
                                                                                                                                                                                                                                                                                                                   PROSITE; PS00021; KRINGLE_1; 4.
PROSITE; PS50070; KRINGLE_2; 4.
Growth factor; Kringle; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
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"Molecular cloning and characterization of cDNA
hepatocyte growth factor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=94060105; PubMed=8241272;
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SIMILARITY: CONTAINS 4 KRINGLE REGIONS.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY
TRYPSIN FAMILY. PLASMINGGEN SUBFAMILY.
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ALTERNATIVE PRODUCTS: A SHORT FORM OF I
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C STRAIN=WISTAR; TISSUE=Liver;

C STRAIN=WISTAR; TISSUE=Liver;

X MEDLINE=91031482; PubMed=2146117;

HSSP; P14210; 2HGF.
MEROPS; S01978; -.
InterPro; IPR000001; -.
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STRAIN-WISTAR; TISSUE-Liver;
MEDLINE-90222197; Pubmed-2139229;
TOShiro K., Hagiya M., Nishizawa
Shimizu S., Nakamura T.;
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01-NOV-1990 (Rel. 16, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
HEPATOCYTE GROWTH FACTOR PRECURSOR (SCATTER FACTOR) (SF)
(HEPATOPOEITIN A).
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P17945;
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                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-sorsend an email to license@isb-sib.ch).
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1;
TRYPSIN FAMILY. PLASMINOGEN SUBFAMILY.
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Pfam; PF00089; trypsin; 1.
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DOMAIN
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                                                         Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases -- -- CATALYTIC ACTIVITY: ATP + H(2)0 = ADP + ORTHOPHOSPH
                                                                                Wiemann S.;
                                                                                                                                         "Characterization of cDNA clones selected by the from size-fractionated cDNA libraries from human DNA Res. 6:329-336(1999).
                                                                                                                                                                                 Ohara O.;
                                                                                                                                                                                         MEDLINE-20039618; PubMed-10574461;
Hirosawa M., Nagase T., Ishikawa K.-I., Kikuno R.,
                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                             Ottenwaelder B., Obermaier B., Mewes H.-W.,
                                                                                                           rissue=Testis;
                                                                                                                      SEQUENCE OF
                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                       Homo sapiens
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                SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
SIMILARITY: BELONGS TO THE CATION TRANSPORT ATPASES FAMILY ATPASES). SUBFAMILY IV.
 SWISS-PROT
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Primates;
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INTERCHAIN (BY SIMILARITY).
N-LINKED (GLCNAC. . .) (POTENTIAL).
M-LINKED (GLCNAC. . .) (POTENTIAL).
MW; 3EOBF1F96ADCEDFF CRC64;
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KRINGLE 3.
KRINGLE 3.
KRINGLE 4.
SERINE PROTEASE-LIKE.
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Pred. No.
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HEPATOCYTE GROWTH FACTOR ALPHA CHAIN
HEPATOCYTE GROWTH FACTOR BETA CHAIN
PYRROLIDONE CARBOXYLIC ACID
                                                                                                                                                                                                                                                                Craniata; Vertebrata; l
Catarrhini; Hominidae;
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Query Match
Best Local Similarity
Watches 5; Conserv
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15-JUL-1998
15-JUL-1998
30-MAY-2000
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the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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DOMAIN
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MEDLINE=97239925; PubMed=908581;

Kopka J., Ludewig M., Mueller-Roeber B.;

"Complementary DNAs encoding eukaryotic-type cytidine-5'-diphosphate-diacylglycerol synthases of two plant species.";

Plant Physiol. 113:997-1002(1997).

-!- FUNCTION: MAY BE INVOLVED IN THE SYNTHESIS OF MINOR PHOSPHOLIPIDS AND IN MODULATION OF 1P3-MEDIATED SIGNAL TRANSDUCTION.

-!- CATALYTIC ACTIVITY: CTP + PHOSPHATIDATE = PYROPHOSPHATE +
                                                                                                                                                                                                                                                       Solanum tuberosum (Potato),
Solanum tuberosum (Potato),
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
                                                                                                                                                                                                                                                                                                                                                 15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
91-MAY-2000 (Rel. 39, Last annotation update)
PHOSPHATIDATE CYTIDYLYLTRANSFERASE (EC 2.7.7.41) (CDP-DIGLYCERIDE SYNTHETASE) (CDP-DIGLYCERIDE PYROPHOSPHORYLASE) (CDP-DIGLYCEROL SYNTHASE) (CDS) (CTP:PHOSPHATIDATE CYTIDYLYLTRANSFERASE) (CDP-DAG SYNTHASE) (CDP-DG SYNTHETASE).
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SEQUENCE
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AL137537; CAB70799.1;
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                                                                                                                                                                    TISSUE-Leaf
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Pred. No.
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MAGNESIUM (BY SIMILARITY).
V; CAF60E3574275AC1 CRC64;
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PHOSPHORYLATION (BY SIMILARITY).
MAGNESIUM (BY SIMILARITY).
MAGNESIUM (BY SIMILARITY).
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EXTRACELLULAR (POTENTIAL).
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TISUE-Skin;
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P43357;
01-NOV-1995
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                                                                                                                                                                                                                                                                            Gaugler B., van den Eynde B., van der Bruggen P., Romero P., Gaforio J.J., de Plaen E., Lethe B., Brasseur F., Boon T.; "Human gene MAGE-3 codes for an antigen recognized on a melanoma autologous cytolytic T lymphocytes."; J. Exp. Med. 179:921-930(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1995 (Rel. 32
15-JUL-1999 (Rel. 38
MELANOMA-ASSOCIATED
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DOMAIN
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Mammalia; Eutheria;
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PATHMAY: PHOSPHOLIFID BIOSYNTHESIS.

SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).

TISSUE SPECIFICITY: ROOTS AND SINK LEAVES.

SIMILARITY: BELONGS TO THE CDS FAMILY.
PROGRESSION. ANTIGEN RECOGNIZED ON A MELANOMA BY AUTOLOG CYTOLYTIC T LYMPHOCYTES.
TISSUE SPECIFICITY: EXPESSED IN MANY TUMORS OF SEVERAL SUCH AS MELANOMA, HEAD AND NECK SQUAMOUS CELL CARCINOMA.
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5; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleotidyltransferase; Phospholipid biosynthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32, Created)
32, Last sequence update)
38, Last annotation update)
ED ANTIGEN 3 (MAGE-3 ANTIGEN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           169
226
226
341
21
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Pred. No. 22;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POLY-ARG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Craniata; Vertebrata;
Catarrhini; Hominidae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    43B556B12F082638 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB
22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (ANTIGEN MZ2-D).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 424
    CARCINOMA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Euteleostomi;
                                                                  AUTOLOGOUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    is
for
    , TYPES
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Best Local S
Matches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P05845;
P05845;
01-NOV-1988 (Rel. 09
01-JAN-1990 (Rel. 19
01-AUG-1992 (Rel. 2
01-AUG-1992 (Rel. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                               This
                                                                                                                                                                                                                   regulatory gene product.";

Nucleic Acids Res. 14:7915-7927(1986).

-!- FUNCTION: TNSABC + TNSD PROMOTE HIGH-FREQUENCY INSERTION OF
INTO A SPECIFIC TARGET SITE KNOWN AS ATT-TN7 WHEREAS TNSABC
PROMOTE LOW-FREQUENCY INSERTION INTO MANY DIFFERENT SITES.
                                                                                                                                                                                                                                                                                                                                       Smith
"Tn7 1
                                          use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                  the
                                                                                                                                                          between
                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. MEDLINE-87040763;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Flores C., Qadri M.I., Lichtenstein C *DNA sequence analysis of five genes; for Tn7 transposition.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE-90192166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Escherichia coli.
Bacteria; Proteob
Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TNSE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TNSE_ECOLI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antigen; Multigene family;
DOMAIN 40 43
MUTAGEN 170 170
MUTAGEN 176 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR002190; -
Pfam; PF01454; MAGE; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U03735; AAA17446.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 IGHLYI 9
                                                                                                          ween the Swiss Institute of Bioinformatics European Bioinformatics Institute. There a by non-profit institutions as long as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CARCINOMA AND BREAST CARCINOMA, BUT NOT FOR TESTES AND PLACENTA. NEVER EXPRESSE LEUKENIAS AND LYMPHOMAS.
SIMILARITY: BELONGS TO THE MAGE FAMILY.
                                                                                                                                                   SWISS-PROT entry is copyright. It is produced through a c
                                                                                                                                                                                                                                                                                                                                  transposition: a multigene process.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IGHLYI 177
    x17693;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          314 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
    CAA35687.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           el. 13, Last sequence update)
el. 23, Last annotation update)
TRANSPOSITION PROTEIN TNSE (PR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  43
170
176
34747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09,
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                                                                                                                                                                                                                                                                                                                                                                                  PubMed=3022239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  18:901-911(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gamma subdivision;
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POLY-SER.

D-A: ABOLISHES HLA-A1 BINDING.

Y-A: ABOLISHES HLA-A1 BINDING.

Y-A: ABOLISHES HLA-A1 BINDING.

MW; 3F5EB13D1C9946A1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 33; DB; Pred. No. 25; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               c.;
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25;
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                                                                http://www.isb-sib.ch/announce/
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                                                                                     Usage
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                                                                                                                                                       outstation
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+ TNSE
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g 29

163 VVRLGHL

169

1 VVRIGHL

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Query Match
Best Local S
Matches 6
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Best Local
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P55931;
01-NOV-1997
01-NOV-1997
01-NOV-1997
                                                        NP_BIND
TRANSMEM
METAL
METAL
METAL
METAL
SEQUENCE
                                                                                                                                                                                                                transfer flavoprotein-ubiquinone oxidoreductase.";
Eur. J. Blochem. 219:277-286(1994).
FUNCTION: ACCEPTS ELECTRONS FROM ETF AND REDUCES UBIQUINONE.
-!- FUNCTION: ACTIVITY: REDUCED ETF + UBIQUINONE = ETF + UBIQUIN
-!- COFACTOR: FAD AND A 4FE-4S CLUSTER.
-!- SUBUNIT: MONOMER (BY SIMILARITY).
-!- SUBUNIT: MONOMER (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOY-1997 (Rel. 35, Created)
01-NOY-1997 (Rel. 35, Last sequence update)
ELECTRON TRANSFER FLAVOPROTEIN-UBIQUINONE OXIDOREDUCTASE PRECURSOR (EC 1.5.5.1) (ETF-QO) (ETF-UBIQUINONE OXIDOREDUCTASE) (ETF
DEHYDROGENASE) (ELECTRON-TRANSFERRING-FLAVOPROTEIN DEHYDROGENASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL, X04534; CAB56509.1; -.
PIR; A2544; OQECD7.
PIR; S12641; S12641.
PIR; S06770; S06770.
Transposable element; Transposition; DNA recombination; DNA-binding.
DNA_BIND
DNA_BIND
311 330 H-T-H MOTIF (BY SIMILARITY).
SEQUENCE 538 AA; 61211 MW; DE34A3F141A1885B CRC64;
                                                                                                                                                  CHAIN
                                                                                                                                                             4Fe-4S;
NON_TER
TRANSIT
                                                                                                                                                                                              Oxidoreductase;
                                                                                                                                                                                                                                                                                                                            MEDLINE=94139702; P
                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9823; [1]
                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                              Sus scrofa
                                                                                                                                                                                                                                                                                                "Molecular cloning and expression of a cDNA encoding
                                                                                                                                                                                                                                                                                                            Frerman
                                                                                                                                                                                                                                                                                                                                                                                                                            ETFDH.
                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                    FRAGMENT).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13
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                                                                                                                                                                                                         SIMILARITY).
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                                                                                                                                                                                   Mitochondrion;
 Similarity 6; Conser
                                                                                                                                                                                                                                                                                                                     S.I., Axtell K.M., Bindoff L.A., Beard S.E.,
                                                                                                                                                                                                                                                                                                                                                                                                             (Pig).
                                                         61
448
551
576
579
582
607
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  Conservative
                                                                                                                                                24
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                                                                                                                                                                                           Electron
                                                                                                                                                                                                                                                                                                                                 PubMed-8306995;
                                                        582
67590
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468
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576
579
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607
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                                                                                                                                                                                                                                                                                                                                                                                        Cetartiodactyla;
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            85
85
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75
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Transit pept
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Pred. No. 50;
1; Mismatches
                                                       POTENTIAL.
IRON-SULFUR (4FE-4S) |
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Pred.
                                                                                                                             FAD
                                                                                                                                     ELECTRON TRANSFER FLAVOPROTEIN-UBIQUINONE OXIDOREDUCTASE.
                                                                                                                                                              MITOCHONDRION (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                 port; Flavoprotein; F.
peptide; Ubiquinone;
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                                                                                                                          (ADP PART)
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No.
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44;
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                       1;
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                                                                                                                          (POTENTIAL)
                      Length 607;
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                                                          CRC64;
                                                                                                                                                                                 FAD; Iron-sulfur
e; Transmembrane.
                                                                   (POTENTIAL)
                                                                                          (POTENTIAL)
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Sus.
                                                                                                                                                                                                                                                                                                                       Gill R.E.,
                                                                                                                                                                                                                                                                                                 human electron
                                                                                                                                                                                             Iron-sulfur;
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Gaps
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GCKR.ZENLA
GCKR.ZENLA
ID GCKR.X
ID GCKR.X
O1154
AC Q91754
AC Q91754
DT 01-NOV
DT 01-NOV
DT 01-NOV
DT 02-NAY
DC GLUCOK
OS Xenopu
OC ENKARY
OC Amphib
OC Xenopo
OX NCBLI
RP SEQUUN
RA Veiga
RT TISSUE
RX MEDLIN
RA Veiga
RT Phospi
RI Eur. J
CC -1-FU
CC
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Best Local Similarity
""" 6; Conservi
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                             SEQUENCE.

SEQUENCE.

SEQUENCE:

MEDLINE-95354920; Pubmed-7628683;

MEDLINE-95354920; Pubmed-7628683;

NOSO T., Lance V.A., Kawauchi H.;

"Complete amino acid sequence of crocodile growth hormone.";

"Complete amino acid sequence of crocodile growth hormone.";

Gen. Comp. Endocrinol. 98:244-252(1995).

-1- FUNCTION: GROWTH HORMONE PLAYS AN IMPORTANT ROLE IN GROWTH

CONTROL AND INVOLVED IN THE REGULATION OF SEVERAL ANABOLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q91754;
Q1.NOV-1997 (Rel. 35, Created)
O1-NOV-1997 (Rel. 35, Last sequence update)
O1-NOV-1997 (Rel. 39, Last annotation update)
30-MAY-2000 (Rel. 39, Last annotation update)
GLUCOKINASE REGULATORY PROTEIN (GLUCOKINASE REGULATOR).
Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOMA_CRONO STANDARD: PRT; 190 AA. P55755; 01-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 01-NOV-1997 (Rel. 35, Last annotation update) SOMATOTROPIN (GROWTH HORMONE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Veiga-Da-Cunha M., Detheux M., Watelet N., van Schaftingen E.;
Veiga-Da-Cunha M., Detheux M., Watelet N., van Schaftingen E.;

"Cloning and expression of a Xenopus liver cDNA encoding a fructose-
phosphate-insensitive regulatory protein of glucokinase.";
Eur. J. Biochem. 225:43-51(1994).

-I- FUNCTION: INHIBITS GLUCOKINASE BY FORMING AN INACTIVE COMPLEX WITH
                                                                                                                                                                                                                                                                                                                                     Crocodylus novaeguineae (Crocodile).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archbasauria; Crocodylidae; Crocodylinae; Crocodylus.
NCBI_TaxID-8503;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001347; -.
InterPro; IPR001741; -.
Pfam; PF01380; SIS; 1.
PROSITE; PS01272; GCKR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X80901; CAA56863.1; -.
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PROCESSES.
SUBCELLULAR LOCATION:
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Pred. No.
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6; Conservative
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PROSITE; PSO0338; SOMATOTROPIN_2;
HORMODE; P1ULITARY;
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DISULFID 180 188 BY SI
SEQUENCE 190 AA; 22008 MW; 7DE
                                                                                                                                                                        InterPro; IPR001400; -
Pfam; PF00103; hormone; 1
PRINTS; PR00836; SOMATOTROPIN.
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BY SIMILARITY.
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                                                                                                                                                                                                 Score
    spTREMBL_16:*
1: sp_archea:*
2: sp_bacteria:
3: sp_fungl:*
4: sp_human:*
5: sp_inverteb:
6: sp_mammaal:*
7: sp_mhc:*
8: sp_organel1:
9: sp_page:*
10: sp_plant:*
11: sp_rodent:
12: sp_unclass
13: sp_vertebr:
14: sp_virus:*
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sp_bacteria:*
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O9nsd3 homo sapien
O9si81 arabidopsis
O49639 arabidopsis
O9vvf8 drosophila
O9sl75 streptomyce
O45454 bacillus su
O64101 bacteriopha
O65815 heianthus
O9rmz0 bacillus an
O16769 mycobacteri
O9udu6 homo sapien
O91n77 arabidopsis
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O91y73 thermotoga
O9esm3 mus musculu
O9esm3 mus musculu
O9esm3 rattus norv
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| • | 64.0 | 64.0 | 64.0 | 64.0 | 64.0 | 64.0 | 66.0 | 66.0 | 66.0 | 66.0 | 66.0 | 66.0 | 66.0 | 66.0 | 66.0 | 66.0 | 66.0 | 66.0 | 66.0 | 68.0 | 68.0 | 68.0 | 68.0 | 68.0 | 68.0 |
| 204 | 199 | 196 | 191 | 176 | 154 | 110 | 1232 | 1112 | 663 | 604 | 444 | 361 | 338 | 337 | 324 | 313 | 301 | 168 | 101 | 1461 | 1288 | 1244 | 1235 | 438 | 363 |
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| Q9PRH7 | 088119 | Q9LP00 | Q9ZVX9 | 087064 | Q9MZA9 | Q49296 | 023998 | Q9UYR7 | Q9RVW5 | Q9V5D9 | 085748 | Q9UWV2 | Q9UWX3 | Q9YFK2 | Q9Z4K0 | 028287 | 052770 | Q9PDR0 | Q9PH51 | Q9SIM3 | Q9STV0 | 082607 | Q9PTG7 | Q9SZ17 | Q9EVH2 |
| Q9prh7 oreochromis | O88119 listeria mo | Q91p00 arabidopsis | Q9zvx9 arabidopsis | O87064 vibrio chol | Q9mza9 ovis aries | Q49296 mycoplasma | က | Q9uyr7 pyrococcus | Q9rvw5 deinococcus | Q9v5d9 drosophila | 085748 treponema d | Q9uwv2 sulfolobus | sulfolobus | Q9yfk2 aeropyrum p | | 028287 archaeoglob | | xylella | Q9ph51 xylella fas | | | O82607 arabidopsis | Q9ptg7 xenopus lae | Q9sz17 arabidopsis | Q9evh2 buchnera ap |

ALIGNMENTS

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| ery Match st Local Sin tches 10; | SEQUENCE | InterPro; I Pfam; PF014 | EMBL; U8267 | and man."; Genome Res. | "Comparativ | Rhodes M., | Kerry G., G | Straw R., W | Nordsiek G. | Mallon A.M. | [1] | NCBI_TaxID= | Mammalia; E | Eukarvota; | Homo sapien | MELANOMA AN | 01-MAR-2001 | 01-OCT-2000 | 01-00T-2000 | Q9NSD3 | D3 |
| vat | 314 AA; 3 | 54; MAGE; | 1; AAF4478 | 0:0-0(200 | e genome s | Denny P., | reystrong | leston P., | , Strivens | , Platzer | | 9606; | | | s (Human). | TIGEN FAMI | | - | | PRELIMINA | |
| .0%; | 4836 MW; | ∴ .' | 9.1; | ō). | equence a | Rosenthal | J.S., Cla | Hunter C. | M.A. KI | M., Bates | | | | | | LY Al2. | 16, | 15 (| 15 | | |
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| | Score 50; DB 4; Pred. No. 0.097; 0; Mismatches | SEQUENCE 314 AA; 34836 MW; 7E00F7CECD8F6568 CRC64; Query Match 100.0%; Score 50; DB 4; Length 314; Best Local Similarity 100.0%; Pred. No. 0.097; Matches 10; Conservative 0; Mismatches 0; Indels | Interero; IPRU0Z190; Pfam; PF01454; MAGE; 1. SEQUENCE 314 AA; 34836 MW; 7E00F7CECD8F6568 CRC64; SEQUENCE 104 AA; 34836 MW; 7E00F7CECD8F6568 CRC64; SEQUENCE 104 AA; 34836 MW; 7E00F7CECD8F6568 CRC64; SEQUENCE 106 AA; Score 50; DB 4; Length 314; Best Local Similarity 100.0%; Pred. No. 0.097; Best Local Similarity 100.0%; Pred. No. 0.097; Matches 10; Conservative 0; Mismatches 0; Indels | EMBL; U82671; AAF44789.1; Interero; IPR002190; Pfam; PF001454; MAGE; 1. SEQUENCE 314 AA; 34836 MW; 7E00E7CECD8F6568 CRC64; SEQUENCE 310 AA; 34836 MW; Score 50; DB 4; Length 314; Best Local Similarity 100.0%; Pred. No. 0.097; Matches 10; Conservative 0; Mismatches 0; Indels | and man."; Genome Res. 0:0-0(2000). EMBL; U82671; AAF44789.1; Interpro; IPR002190; Pfam; PF01454; MAGE; 1. SEQUENCE 314 AA; 34836 MW; 7E00F7CECD8F6568 CRC64; SEQUENCE 314 AA; 34836 MW; Score 50; DB 4; Length 314; Best Local Similarity 100.0%; Pred. No. 0.097; Matches 10; Conservative 0; Mismatches 0; Indels | "Comparative genome sequence analysis of the Bpa/Str region and man."; Genome Res. 0:0-0(2000). EMBL; U82671; AAF44789.1; Interpro; IPR002190; Pfam; PF01454; MAGE; 1. SEQUENCE 314 AA; 34836 MW; 7E00F7CECD8F6568 CRC64; SEQUENCE 314 AA; 34836 MW; PE00F7CECD8F6568 CRC64; SEQUENCE 314 AA; 34836 MW; PE00F7CECD8F6568 CRC64; SEQUENCE 314 AA; 34836 MW; Pred. No. 0.097; Best Local Similarity 100.0%; Pred. No. 0.097; Matches 10; Conservative 0; Mismatches 0; Indels | Que Bes Mat | Que Bes Mat | Que | Que | Que Mat | Mat | Ωue Bes | Mat C | Mat | Mac | Mac S C C C C C C C C C C C C C C C C C C | Mat S | Mat S | Mac de Servicio de la Companya de la | Mac e |

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01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence
01-OCT-2000 (TrEMBLrel. 15, Last annotati
CDP-DIACYLCLYCEROL SYNTHETASE-LIKE PROTEI
T10114.170 OR AT4G22340.
Arabidopsis thaliana (Mouse-ear cress)
Eukaryota; Viridiplantae; Embryophyta; Tr
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SEQUENCE FROM N.A.

Walker M., Shinn P., Brooks S., Buehler E., Chao Q., Dummer M., Schinn P., Brooks S., Buehler E., Chao Q., Dummer A., Kam C., Altafi H., Araujo R., Conn L., Conway A.B., Gonzalez A., Kam C., Altafi H., Lenz C., Li J., Liu S., Hansen N.F., Huizar L., Kremenetskala I., Lenz C., Li J., Liu S., Luros S., Rowley D., Schwartz J., Torlumi M., Vysotskala V., Yu G., Davis R.W., Federspiel N.A., Theologis A., Ecker J.R.;

Davis R.W., Federspiel N.A., Theologis A., Ecker J.R.;

"Commic sequence for Arabidopsis thaliana BAC F23N19 from chromosome
                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
Bevan M., Murphy G., D
Bancroft I., Mewes H.W
Submitted (FEB-1998) t
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01-MAY-2000
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F23N19.5.
                                                                                                             Mendel; 2000, 174; -. InterPro; IPR000374; -. Pfam; PF01148; Cytidylyltrans; PROSITE; PS01315; CDS; 1. PROSITE; PS01315; CDS; 1. 48247 MW;
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SEQUENCE
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Bukaryota; Viridiplantae; Embryophyta; Trachec
Magnoliophyta; endicotytedons; core eudicots;
Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
                                                                                                                                                                    EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
EMBL; ALIG1712; CAA16784.1; -.
EMBL; ALIG1557; CAB79189.1; -.
Mendel; 28363; Arath;2834;28363.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                            sequence update)
annotation updat
KE PROTEIN.
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No:
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15;
                                                                 66;
                                                                                                                                                                                                                                                                                                                                                                      Tracheophyta;
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                                                                                                                                                                                                                                                                                          Hudson S., Ridley
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                                                                                                                                                                                                                                                                  databases
                                                                                                                                                                                                                                                                                                                                                            Rosidae;
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                                                                            Length 423;
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e; eurosids II;
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                                                                                                                            Matches
                                                                                                                                                    Query Match
Best Local
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Q9VVF8;
Q1-MAY-2000 (TrEMBLrel. 13, Created)
Q1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
Q1-MAY-2000 (TrEMBLrel. 13, Last annotation update)
Q1-MAY-2000 (TrEMBLrel. 13, Last annotation update)
Q67692 PROTEIN.
Q67692.
Q7692.
Q76
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   216
                                                            1 VVRIGHLYIL
   ITLIGHLYLL
                                                                                                                      6; Conserv
                                                                                                                            Conservative
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                                                                                                                      Score 36; DB Pred. No. 2.2e 2; Mismatches
                                                                                                                                                           DB 5;
2.2e+02
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                                                                                                                                                                                      Length 1310
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RESULT Q9S1R5

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  Query Match
Best Local S
Matches 6
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Q45454;
Q45454;
Q45454;
T01-NOV-1996 (TrEMBLrel. 01, Created)
T01-NOV-1996 (TrEMBLrel. 02, Last sequence update)
T01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
E PROBABLY POSITIONED IN OPERON WITH DOWNSTREAM ORF5.
Bacillus subtilis.
S Plasmid pTA1060.
Bacillus/Staphylococcus group; Bacillus.
C Bacillus/Staphylococcus group; Bacillus.
C NCBL_TaxID=1423;
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Best Local Similarity
Matches 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Redenbach M., Kieser H.M., Denapaite D., Eichner A., Kinashi H., Hopwood D.A.;
"A set of ordered cosmids and a detailed genetic and the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1995).
EMBL, AL109972; CAB53266.1; -.
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Streptomyces coelicolor.

Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                 STRAIN-A3(2);
MEDLINE-97000351; PubMed-8843436;
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NCBI_TaxID=1902;
[1]
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                                                                                                                                                                                                                                              MEDLINE-95206941; PubMed-7899081;
Meijer W.J., Venema G., Bron S.;
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                                                                                                                                                        EMBL;
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U32380; AAC44422.1;
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Similarity 66. 6; Conservative
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                     70.0%;
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e EMBL/GenBank/DDBJ databases.
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Score 35; DB
Pred. No. 73;
2; Mismatches
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2;
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                                                                                                               DB410B2A7BC51B22
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                                           DB
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  1.
                                         Length 305
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  Indels
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RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Foulger D., Emmerson P.T.,
RA Gliseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Gliseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Kurlta K., Lapidus A., Lardinois S., Kullan G., Kumano M.,
RA Kurlta K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Kurlta K., Lapidus A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Kurlta K., Lepidus A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Noone D., O'Reilly M., Portetelle D., Porwollk S., Prescott A.M.,
RA Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
RA Satio T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Setiguchi J., Sekowska A., Serror S.J., Serror P., Shin B.S., Soldo B.,
RA Takeuchi M., Tamakoshi A., Taranaka T., Terpstra P., Tognoni A.,
RA Yoshida K., Wambutt R., Wedler E., Wedler H., Weitzenegger T.,
RA Winters P., Willey A., Yamanot C. H., Yasamoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;
RT Subtilis P., Park S., Park S., Park S.,
                                                                           Query Match
Best Local S
Matches 6
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01-JAN-1998
01-JAN-1998
01-NOV-1998
                                                                                                                                                                            Kunst F., Ogasawara N., Yoshikawa H., Danchin Submitted (NOV-1997) to the EMBL/GenBank/DDBJ EMBL; 299114; CAB13971.1; -. EMBL; 299115; CAB13997.1; -. SEQUENCE 325 AA; 37571 MW; EB73F9970BC5ACC
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Bacteria, Firmicutes, Baccillus/Clostridium group;
Baccillus/Staphylococcus group; Baccillus.
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MEDLINE-98044033;
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                                                                         70.0%; milarity 75.0%; Conservative
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B (TrEMBLrel. 05,
B (TrEMBLrel. 08,
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Last sequence update)
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                                                                           Score 35; DB Pred. No. 79; 1; Mismatches
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01-AUG-1998
01-AUG-1998
01-AUG-1998
                                                                                                                                           "Cloning, expression in yeast, and functional characterization of CYP8IB1, a plant cytochrome P450 that catalyzes in-chain hydroxylatio of fatty acids.",
    of fatty acids.",
    of fatty acids.",
    J. Biol. Chem. 273:7260-7267(1998).
    -1- FUNCTION: CATALYZES THE HYDROXYISOFLAVONES, 2'-HYDROXYDAIDZEIN AND 2'-HYDROXYFORMONOMETIN, RESPECTIVELY (BY SIMILARITY).
    AND 2'-HYDROXYFORMONOMETIN, RESPECTIVELY (BY SIMILARITY).
    -1- CATALYTIC ACTIVITY: FORMONOMETIN + NADPH + O(2) =
    -2'HYDROXYFORMONOMETIN + NADPH + O(2) -
    -1- COPACTOR: THE ENZYME IS NADPH-DEPENDENT.
    -1- COPACTOR: THE ENZYME IS NADPH-DEPENDENT.
                                                                                                                                                                                                                                                                                                                                                                                                        O65815 PRELIMINARY; PRT; 520 AA.

O65815; O65814;

01-AUG-1998 (TrEMBLrel. 07, Created)

01-AUG-1998 (TrEMBLrel. 07, Last sequence update)

01-AAR-2001 (TrEMBLrel. 16, Last annotation update)

CYTOCHROME P450 81B1 (EC 1.14.13.53) (ISOFLAVONE 2'-YFOR CYP81B1 OR CYP81B1C OR CYP81B1S.

Helianthus tuberosus (Jerusalem artichoke).

Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spe Magnollophyta; endicotyledons; core endicots; Asteridae; enasterids II; Asterales; Asteraceae; Asteroideae; Helia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
Lazarevic_V., Duesterhoeft
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteriophage SPBc2.
Viruses; dsDNA viruses,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (AUG-1997) to the EMBL; AF020713; AAC13061.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HYPOTHETICAL YOPR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              064101
                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-CV. BLANC COMMUN; TISSUE-TUBER;
MEDLINE-98184826; PubMed=9516419;
Cabello-Hurtado F., Batard Y., Salaun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein. seQUENCE 325 AA; 37571 MW;
InterPro; IPR001128; -. P2am; PF00067; p450; 1. PRINTS; PR00385; P450.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Karamata D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=66797;
                                                                                             <del>-</del>
                                                                                                                                                                                                                                                                                                 Werck-Reichhart D.;
                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=4233;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Match
                                     PATHWAY: INVOLVED IN THE BIOSYNTHESIS OF ISOFLAVONOID-E ANTIMICROBIAL COMPOUNDS OF LEGIMES.

ALTERNATIVE PRODUCTS: TWO FORMS; CYP81B1L (SHOWN HERE) CYP81B1S; ARE PRODUCED BY ALTERNATIVE SPLICING.

SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.

L; AJ000477; CAA04116.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                                                                                                                                  AMINOPURINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IVRSGHLY 263
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6; Conser
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(TrEMBLrel.
L 37.6 KDA PR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RNA stage;
                                                                                                                                                                                                                                                                    st, and functional characterization of P450 that catalyzes in-chain hydroxylation
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Pred.
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                                                                                                                                                                                                                                                                                                              Salaun J.-P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EB73F9970BC5ACC3 CRC64
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79;
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                                                                                                                       ISOFLAVONOID-DERIVED
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                                                                                                                                                                                                                                                                                                                Pinot F.,
                                                                                                                                                                                                                                 DAIDZEIN AND
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ID O06769
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AC O0
DT O0

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Best Local
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Best Local
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                                                                                                                                                                      O06769 PRELIMINARY; PRT; 637
O06769; O1-JUL-1997 (TIEMBLIEL 04, Last sequence of JUN-2000 (TIEMBLIEL 14, Last annotate hypothetical 69.5 KDA PROTEIN.

RV0669C OR MIT376.05.

Bacteria; Firmicutes; Actinobacteria; Actinobact
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

OKinaka R.T., Cloud K., Hampton O., I
OKinaka R.T., Cloud K., Hampton O., I
Kumano S., Manter D., Martinez Y., S'
Brown A.E., Jackson P.J.;
Brown A.E., Jackson P.J.;
Brown A.E., Jackson P.J.;
Submitted (NOV-1999) to the EMBL/Gen
EMBL; AR18935, AAF13647.1;
InterPro; IPR0011119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9RMZ0;
Q9RMZ0;
01-MAY-2000
01-MAY-2000
01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NADP.
BINDING
VARSPLICT
CONFLICT
CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF01520;
Plasmid.
SEQUENCE 531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro;
InterPro;
                                                                     Actinomycetales;
NCBI_TaxID=1773;
[1]
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Oxidoreductase;
   SEQUENCE FROM STRAIN=H37RV;
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|:||:||:|
467 VKIGNLYVL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pro; IPR002508;
PF00395; SLH;
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                                                                                                                                               Corynebacterineae;
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85.7%;
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16,
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MISSING (IN CYP81B1S).
MISSING (IN CAA04116).
Y -> S (IN CAA04116).
P -> Q (IN CAA04116).
P -> Q (IN CAA04116).
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Last sequence update)
Last annotation updat
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Last annotation updat
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                                                                                                                                           Mycobacteriaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               637
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1.3e+02;
0;
                                                                                                                                                                                 Actinobacteridae;
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1.3e+02;
hes 0;
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A Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
AR Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,
AR Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
AR Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
AR Davies R., Devlin K., Feltwell T., Gentles S., Hanlin N., Holroyd S.,
AR Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
AR RA, Colver S., Osborne J., Quall M.A., Rajandream M.A., Rogers J.,
AR RA, Rutter S., Seeger K., Skelton S., Squares S., Sqares R., Sulston J.E.,
AR RA, Taylor K., Whitchead S., Barrell B G.,
AR Raylor K., Whitchead S., Barrell B G.,
AR Rogers J.,
AR Paylor K., Whitchead S., Barrell B G.,
AR Rogers J.,
AR Paylor K., Whitchead S., Barrell B G.,
AR Rogers J.,
AR Paylor K., Whitchead S., Barrell B G.,
AR Rogers J.,
AR Paylor K., Whitchead S., Barrell B G.,
AR Rogers J.,
AR Rogers
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Best Local
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                                                 Pfam; PF00024; PAN; 1.
Pfam; PF00051; kringle; 4.
Pfam; PF00089; trypsin; 1.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00772; CHYMOTRYPSIN.
PRINTS; PR00018; KRINGLE.
PROSTTE; PS00021; KRINGLE_1; UNI
PROSTTE; PS00070; KRINGLE_2; 4.
SMART; SM00020; Tryp_Spc; 1.
                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000001; -.
InterPro; IPR000327; -.
InterPro; IPR001254; -.
InterPro; IPR001314; -.
InterPro; IPR003014; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SIMILARITY: 1
-!- SIMILARITY: 1
EMBL; AC004960; 2
HSSP; P14210; 181
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O9UDU6;

01-MAY-2000 (TrEMBLrel. 13,

01-MAY-2000 (TrEMBLrel. 16,

01-MAR-2001 (TrEMBLrel. 16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

Courtney L., Elliot G., Angell S.;

"The sequence of Homo sapiens PAC clone RP5-1098B1.";

submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (DEC-1999)
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6; Conserv
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637 AA; 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1999) to the EMBL/GenBank/DDBJ databases.
TO SERINE PROTEASES, TRYPSIN FAMILY.
TO CHYMOTRYPSIN SERINE PROTEASE FAMILY (:
AAC71655.1;
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Primates;
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                                                                                                                                   UNKNOWN_4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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       627B1EF99FAD931B CRC64;
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1.6e+02;
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Best Local S
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Best Local
09JLQ1
09JLQ1;
01-0CT-2000
01-0CT-2000
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01-OCT-2000
01-OCT-2000
                                                                                                                                                                                                               SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

Brooks S., Buehler E., Chao Q., Johnson-Hopson C Khan S., Kim C., Altafi H., Bei B., Chin C., Chiou J., Choi E., Con L., Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsky N., Myyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N., Theologis A., Ecker J.;

Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AC022464; AAR79556.1;

SEQUENCE 808 AA; 90243 MW; 6288C800CFIAE04F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Khan S.

Kim C., Altafi H., Bei Q., Chin C., Chiou J., Choi E., Conn L.,

Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B., Lee J.

Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N., Nguyen M.,

Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A.,

Toriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A.,

Ecker J.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Sp. Magnoliophyta; eudicotyledons; core eudicots; Rosidae; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (FEB-2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana (Mouse-ear cress)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                         Submitted
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                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM
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                                                                                                                 1 VVRIGHLYIL
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                                                                                                    VLRIGOLFIL
                                                                                                                                                     Similarity 7; Conserv
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5; Conser
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0 (TrEMBLrel. 15,
1 (TrEMBLrel. 16,
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                                                                                                                                                       Conservative
                                       PRELIMINARY;
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Pred. No.
                                                                                                                                                                Score 35;
Pred. No.
                                                                                                                                                       Mismatches
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                                                                                                                                                                DB 10
2e+02;
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Q49122;
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Q1-NOV-1996 (TrembLrel. 01, Created)
Q1-NOV-1996 (TrembLrel. 01, Last sequence update)
Q1-NOV-1996 (TrembLrel. 16, Last annotation update)
MAU GENE CLUSTER, METHYLAMINE DEHYDROGENASE LARGE AND SMALL SUBUNITS,
AND AMICYANIM, (MAUGHEDACIGIAN) GENES, COMPLETE CDS (FRAGMENT).
Methylobacterium extorquens.
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Methylobacterium group; Methylobacterium.
                                                                                                                                                                                                                    STRAIN=AM1;
STRAIN=94292425; PubMed=8021187;
Chistoserdov A.Y., Chistoserdova L.V., McIntire W.S., Lidstrom M.E.;
"Genetic organization of the mau gene cluster in Methylobacterium extorquens AM1: complete nucleotide sequence and generation and characteristics of mau mutants.";
J. Bacteriol. 176:4052-4065(1994).
EMBL; L26406; AAB46931.1; -.
Pfam; PF01381; HTH_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matsushita M.;
Submitted (MAY.1999) to the EMBL; AF149013; AAF73131.1;
InterPro; IPRO02111; -...
InterPro; IPRO02153; -...
                                                                                                                                                                                    SMART; SM00530; HTH_XRE; 1.

NON_TER 139 139

SEQUENCE 130 **
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=408;
[1]
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letazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
letazoa; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                     Conservative
             June
             20,
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55.6%;
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Pred. No. 50;
3; Mismatches
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Pred. No. 4.9e+02;
4; Mismatches 1;
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13.748 Million cell updates/sec
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MAGE-21 nonapeptid
MAGE-21 nonapeptid
Immunogenic peptid
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Immunogenic peptid
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| n hepatocyte ains alpha- | = | Human hepatocyte g | hepatocyte | - | Human leukocyte-de | Human plasminogen- | | mutant having | <pre>cytotoxi</pre> | modified | modified t | wild-type | | inant hum | TCF-II. Ho | Ω. | nogen-like | ytoto | <u>a</u> | т. | | Amino acid sequenc | m articho | oma pro | XVII | thali | thali | is thali | is thali | is thali | is thali | S |

ALIGNMENTS

RESULT R50283

R50283 standard; Protein; 9 AA.

MAGE-21 nonapeptide 26-SEP-1994 (first entry)

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ACC CARRELL CONTRACTOR CONTRACTOR
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26-MAR-1993;
07-JUN-1993;
                                 WPI; 1994-100844/12.
N-PSDB; Q44753.
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histocompatability; human leucocyte antigen; probe; treatment;
                                                                                                                                                                    Van Derbruggen P;
                                                                                                                                                                                                                Boon-falleur T,
                                                                                                                                                                                                                                                                                                       (LUDW-) LUDWIG INST CANCER RES
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93US-0037230.
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RESULT RE
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R99343-R99350 represent MAGE nonapeptides, based on the tumour rejection antigen region of the full length MAGE sequences. These peptides were used to design the nonapeptides of the invention (see R99337-R99342), which bind to a HIA molecule on a cell, and provoke lysis by cytolytic T cells (CTLs) specific for a complex of the HIA molecule and nonapeptide. The nonapeptides can be used diagnostically to identify tumours expressing a particular HIA molecule, or to identify cancer cells. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            An isolated nonapeptide having the amino acid sequence Glu-Val-Asp-
pro-Ile-Gly-His-Leu-Tyr is derived from the tumour rejection antigen
precursor encoded by the MAGE-3 gene and presented by HIA-Al. The
nonapeptide can be used in a vaccine to treat a cancerous condition
involving HIA-Al subtype cancerous cells. The nucleic acid encoding
the nonapeptide can be used as a probe to identify tumour cells.

This sequence is homologous to the peptide described and is encoded
                                                                                                                                                                                                                                                                                                                                    New nona:peptide(s) that bind to HLA molecule(s) by specific cytolytic T cells, for diagnosis and tumours and to expand T cells in vitro.
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                                                                                                                                                                                                                                                                 Example 4; Fig 4; 41pp; English
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Traversari C, V
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)en Eynde B,
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3.2e+05;
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Van Dei
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                                                                                                                                                                                                                                                                                                                                                                          and induce lysis treatment of
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RESULT
Y46062
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            peptides can also be used therapeutically, to induce a CTL response to tumours (where the peptides are optionally coupled to tumour-specific antibodies), or to induce a response by CTLs that are otherwise inactive. The peptide sequences may also be used to expand specific CTLs in vitro for later return to the patient, such as for treating melanoma. Tumour cells can be identified by using DNA encoding the nonapeptides as probes. Non-human cells transformed with the HLA-Al gene and a DNA sequence encoding one of the peptides, can be used to generate CTLs, or to detect the presence of CTLs in human samples. The non-human transformed cells, when polytransformed, are universal effector cells, and can be used in vaccines, or for treating melanoma or breast cancer.
                                        Y45390 to Y48214 represent specifically claimed immunogenic peptides having a human major histocompatibility complex (MHC) Class I (also known as human leukocyte antigen (HLA) binding motif. The immunogenic peptides can bind to a specific HLA allele (i.e. HLA-A subtypes HLA-A2.1, A1, A3.2 or A24.1 or HLA-B or C) and induce a cytotoxic T cell response against the antigen from which the peptide is derived. Cytotoxic T lymphocytes (CTLs) which destroy antigen-bearing cells are normally induced by an antigen in the form of a peptide fragment bound to a HLA molecule, rather than the intact foreign antigen itself, and
are particularly important in tumour rejection and in fighting viral infections. The peptides are therefore useful therapeutically to tre
                                                                                                                                                                                                                                                                                                                                                                                                       WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sette A,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA immune response; T cell activation; major histocompatibility complex; cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cance prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Y46062 standard; Peptide;
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                                                                                                                                                                                                                                                                                                                                immunogenic peptides with HLA binding motif, useful diagnosis of cancers and viral diseases -
                                                                                                                                                                                                                                                                                                                                                                                                       1999-551214/46.
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8; Conservative
                                                                                                                                                                                                                                                                                     Page 54; 150pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             peptide having a human leukocyte antigen binding
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                                                                                                                                                                                                                                                                                     English.
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Pred. No.
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Best Local S
Matches 8
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This peptide is a tumour rejection antigen presented by a HLA-B44 molecule and derived from a MAGE-12 tumour rejection antigen precursor (TRAP). Claimed tumour rejection antigens (W2308-43) are able to bind to HLA-B44 positive cells, making them useful in identifying cells which present HLA-B44 molecules on their surfaces for use in the diagnosis and therapy of cellular abnormalities. The complex of the tumour rejection antigen and HLA molecule provokes a cytolytic T cell response. The tumour rejection antigens and HLA-B44, can be used as vaccines to treat disorders characterised by expression of the TRAP molecule such as cancer, especially melanoma. Vaccines can also be prepared from cells which present the tumour rejection antigens and answer the tumour rejection antigens are such as cancer.
                                                                                                                                                                                                                                                Tumour rejection antigens presented by molecules - useful to identify HLA-B44 and therapy of cellular abnormalities
                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               melanoma; therapy;
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8; Conservative
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Pred. No.
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                                                                                                                                                                                                                                                                 human leukocyte antigen 844 positive cells for diagnosis
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CC Y45390 to Y48214 represent specifically claimed immunogenic peptides CC having a human major histocompatibility complex (MHC) Class I (also CC known as human leukocyte antigen (HLA)) binding motif. The immunogenic CC peptides can bind to a specific HLA allele (i.e. HLA-A subtypes CC HLA-A2.1, A1, A3.2 or A24.1 or HLA-B or C) and induce a cytotoxic T cell CC response against the antigen from which the peptide is derived. CC Cytotoxic T lymphocytes (CTLs) which destroy antigen-bearing cells are CC normally induced by an antigen in the form of a peptide fragment bound CC are particularly important in tumour rejection and in fighting viral CC infections. The peptides are therefore useful therapeutically to treat CC or prevent viral infections and cancers in mammals (especially humans) CC e.g. prostate cancer, hepatitis B and C, AIDS, and renal carcinoma. CC Individuals susceptible or otherwise at risk of viral infection or CC cancer, or used to treat chronic or acute conditions. They are also CC useful diagnostically, and can be used to induce a cytotoxic T cell cresponse, by contacting a cytotoxic T cell with the peptide e.g. to CC produce CTLs ex vivo for infusion back into a patient. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        as non-proliferative cancer cells and non-proliferative transfectants.
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8; Conser
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26-APR 1999

06-APR 1999

06-APR 1999

16-APR 1999

11-APR 1999

21-APR 1999

22-APR 1999

23-APR 1999

24-MAY 1999

25-MAY 1999

26-MAY 1999

27-MAY 1999

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21-MAY 1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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Pred. No. 0.17;
0; Mismatches
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      04-JUN-1999
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  9908-0137502
9908-0138744
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06-AUG-1999; 06-AUG-1999; 09-AUG-1999; 09-AUG-1999; 10-AUG-1999;

13-AUG-1999; 16-AUG-1999; 17-AUG-1999;

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Gaps

0;

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Best Local Similarity
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990S-0151065

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990S-0151065

990S-0151130

990S-0151130

990S-0151263

990S-015263

990S-0153758

990S-0154739

990S-0155659

990S-0155659

990S-0155659

990S-0157753

990S-0157753

990S-0158232

990S-0159234

990S-0159234

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990S-0160767

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990S-0160767

990S-0160768

990S-0160769

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990S-0161404

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990S-0161361

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990S-0161361
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990S-01474163

990S-0147493

990S-0148171

990S-0148811

990S-0148811

990S-0148664

990S-0149175

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  72.0%;
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Pred.
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            Length 363;
  RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 G13456;
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                                               72.0%;
                                     Score 36; DB Pred. No. 15; 2; Mismatches
                                                        21;
                                                        Length 365;
                                       0,
                                      Gaps
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| 990S-0135533. 990S-0135533. 990S-0135629. 990S-0136782. 990S-0137528. 990S-0137528. 990S-0137524. 990S-0138640. 990S-0138647. 990S-0139452. 990S-0139452. 990S-0139453. 990S-0139453. 990S-0139454. 990S-0139454. 990S-0139455. 990S-0139455. 990S-0139456. 990S-0139458. | 848080W14741Q440888880W11107646 | d; Protei first ent aliana pr fication; assay; ge quence. aliana. 000EP-030 |
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RESULT
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Best Local S
Matches 6
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23-AUG-1999
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25-AUG-1999
27-AUG-1999
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                                                  standard;
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 (first entry)
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9908-0149929
9908-0150864
9908-0151086
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9908-01565931
9908-01565931
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                                                  Protein;
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66.7%;
                                                    369
                                                                                                                                                                 ; Score 36; DB
; Pred. No. 15;
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HORRER REPRESENTATION OF REPRE
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| 0741. 0767. 0768. 0770. | 584. | 329. | 294. | 369. | 865. | 117. | 458. | 7 8 6 V | 779. | 018. | 070. | 930. | 303 | 065. | 884. | 930. | 929. | 722. | 175. | | 319. | | 416. | 260. | 302. | 038. | 388. | 951. 386. | 918. 919. | 276. 913. | 218. | 192. |
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ALIGNMENTS

C;Species: Homo_saplens (man) C;Date: 07-Jun-1996 #Sequence_revision 07-Jun-1996 #text_change 18-Feb-2000 C;Accession: I74519; JC2362; PH1295 R;De Smet, C:; Lurquin, C:; van der Bruggen, P.; De Plaen, E:; Brasseur, F:; Boon, T. Immunogenetics 39, 121-129, 1994 A;Title: Sequence and expression pattern of the human MAGE2 gene. A;Accession: I74519 A;Accession: I74519 A;Molecule type: mRNA A;Residues: 1-9,'S',11-186,'D',188-299,'S',301-314 <DIN> A;Residues: 1-9,'S',11-186,'D',188-299,'S',301-314 <DIN> A;Residues: 1-9,'S',11-186,'D',188-299,'S',301-314 <DIN> A;Experimental source: melanoma cell line DM150; MAGE-12f R;Traversari, C.; van der Bruggen, P.; Luescher, I.F.; Lurquin, C.; Chomez, P.; Var. P J. Exp. Med. 176, 143-1457, 1992 A;Title: A nonapeptide encoded by human gene MAGE-1 is recognized on HLA-A1 by cytoly A;Reference number: PH1294; MUID:93018875 A;Accession: PH1294; MUID:93018875 A;Cross-references: GB:L18877; NID:g499345; PIDN:AAA19023.1; PID:g499346 R;Ding, M.; Beck, R.J.; Keller, C.J.; Fenton, R.G. Biochem. Biophys. Res. Commun. 202, 549-555, 1994 A;Title: Cloning and analysis of MAGE-1-related genes. A;Reference number: JC2358; MUID:94311935 A;Accession: JC2362 A;Map position: Xq28-Xq28 C;Superfamily: tumor associated protein MAGE F;168-176/Region: HLA-Al binding #status predicted A;Gene: GDB:MAGEA12; MAGE12; MAGE-12f A;Cross-references: GDB:331129 A;Status: preliminary; translated from GB/EMBL/DDBJA;Molecule type: DNA A;Residues: 1-314 <DES> melanoma antigen MAGE-12 - human N;Alternate names: MAGE 21 prote C; Genetics: A; Experimental source: MAGE-21 A; Molecule type: DNA A; Residues: 168-176 <TRA> Matches Query Match Best Local 170 VRIGHLYIL 178 1 VRIGHLYIL similarity 100.0%; 9; Conservative 0 9 protein 0; Score 46; DB 2; Pred. No. 0.085; Mismatches DB 2; Length 314; Indels 0; Gaps 0;

RESULT B96652

protein F23N19.5 [imported] - Arabidopsis thaliana

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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: B96652
R;Theologis, A; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Liuros, J.S.; Maiti, R.; Marzia Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Reference number: A86141; MUID:21016719
A;Accession: B96652
A.;Accession: B96652
hypothetical protein 4.60 - Bacillus subtilis plasmid pTA1060 c; Species: Bacillus subtilis c; Scate: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 24-Nov-1999 c; Accession: I40565 pton, S. Nucleic Acids Res. 23, 612-619, 1995 pton, S. Nucleic Acids Res. 23, 612-619, 1995 pton, Status: Characterization of single strand origins of cryptic rolling-circle plasmids A; Reference number: I40549; MUID:95206941 pton GB/EMBL/DDBJ preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   probable membrane protein - Streptomyces coelicolor C;Speciaes: Streptomyces coelicolor C;Speciaes: Streptomyces coelicolor C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999 C;Accession: T37141
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A: Gene: F23N19.5
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A; Residues: 1-234 <HAR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Gene: F23N19.5
A; Map position: 1
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A; Residues: 1-233 <STO>
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                                                            A; Didus, Free DNA A; Molecule type: DNA A; Molecule type: DNA A; Residues: 1-613 <STO> A; Residues: 1-613 <STO> A; Cross references: GB:BA000008; NID:g8978745; PIDN:BAA98581.1; GSPDB:GN00142 A; Cross references: Strain J138
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C; Superfamily: Bac
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A; Molecule type: DNA
A; Residues: 1-305 <RES>
A; Cross-references: EMBD:U32380; NID:g1049123; PIDN:AAC44422.1; PID:g1049128
A; Experimental source: plasmid pTA1060
C; Genetics:
A;Description: specifically catalyzes the hydroxylation of medium chain saturated fat C;Superfamily: human cytochrome p450 CYP2D6; cytochrome p450 homology C;Keywords: chromoprotein; fatty acid metabolism; heme; iron; metalloprotein; oxidore F;301-463/homain: cytochrome p450 homology <P45> F;441/Binding site: heme iron (Cys) (axial ligand) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  J. Biol. Chem. 273, 7260-7267, 1998
A;Tittle: Cloning, expression in yeast and functional characterization of CYP81B1, a p A;Reference number: Z17204; MUID:98184826
A;Accession: T10896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary; translated from GB/EMBL/DDBJA;Molecule type: mRNAA;Residues: 1-505 <CAB>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cytochrome P450 (EC 1.14. -. ) 81B1c - Jerusalem artichoke
C;Species: Helianthus tuberosus (Jerusalem artichoke)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Feb-2001
C;Accession: T10896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Cabello-Hurtado, F.; Batard, Y.; Salaun, J.; Durst, F.; Pinot, J. Biol. Chem. 273, 7260-7267, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:AJ000477; NID:g3059128; PIDN:CAA04116.1; A;Experimental source: cv. blanc commun
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85.7%;
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66.7%;
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Pred. No.
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Pred.
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26;
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                                                                                               M.; Kishi, F.; Ouchi, K.; Shiba,
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                                                                                                                                        #text_change 02-Mar-2001
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pneumoniae

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A;Cross-references: GB:295972; GB:AL123456; NID:g3261790; A;Experimental source: strain H37Rv C;Genetics:
                                                                                                                                                                                                                                                                     R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; H. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the comple A;Reference number: A70500; MUID:98295987
A;Accession: H70535
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C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-May-2000
C;Accession: E72087; D81582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A:Title: Comparative genomes of Clamydia pneumoniae A;Reference number: A72000; MUID:99206606 A;Accession: E72087
                                                                                           A; Gene: Rv0669
C; Superfamily:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein Rv0669c - Mycobacterium tuberculosis (strain H37RV) c;Species: Mycobacterium tuberculosis C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000 C;Accession: H70535
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A;Residues: 1.613 <REA>
A;Cross-references: GB:AE002200; GB:AE002161;
A;Experimental source: strain AR39, HL cells
C;Genetics:
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A; Residues: 1-637 <COL>
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A; Residues: 1-613 <ARN>
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    Query Match
Best Local Similarity
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Best Local
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                                                                                           Mycobacterium tuberculosis hypothetical
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87.58;
    73.98;
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Pred. No.
    Score 34;
Pred. No.
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DB
54;
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                          Length
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                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 1-728 <MIY>
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A;Accession: A36677
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A; Accession: JU0333
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A; Residues: 1-728 <SEK>
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                                                                                                                                                                                  A;Accession: A39006
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A; Residues: 1-728 <SE3>
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C;Species: Homo sapiens (man)
C;Date: 17-Aug-1992 #sequence_revision 17-Aug-1992 #text_change 08-Dec-2000
C;Accession: JH0579, JU0333; A41140; B36677; A36677; A33512; A39006; PH0114; A37796; R;Seki, T.; Hagiya, M.; Shimonishi, M.; Nakamura, T.; Shimizu, S.
Gene 102, 213-219, 1991
A;Experimental source: embryonic lung R;Yoshiyama, Y., Arakaki, N.; Naka, D.; Takahashi, K.; Hirono, Biochem. Biophys. Res. Commun. 175, 660-667, 1991 A;Title: Identification of the N-terminal residue of the heavy A;Reference number: PH0114; MUID:91207365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Experimental source: leukocyte
R; Miyazawa, K.; Tsubouchi, H.; Naka, D.; Takahashi, K.; C
Biochem. Biophys. Res. Commun. 163, 967-973, 1989
A; Title: Molecular cloning and sequence analysis of cDNA
A; Reference number: A33512; MUID:89392017
A; Accession: A33512
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A;Residues: 1-481,'RT',484-728 <SE2>
A;Residues: K.M.; Arakaki, N.; Hartmann, G.; Vandekerckhove,
Proc. Natl. Acad. Sci. U.S.A. 88, 7001-7005, 1991
A;Title: Evidence for the identity of human scatter factor &
A;Reference number: A41140; MUID:91334393
A;Accession: A41140
A;Molecule type: mRNA
A;Residues: 1-728 <MEI>
A;Residues: 1-728 <MEI>
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A;Note: the authors translated the codon GAA for residue 662 a.
R;Seki, T.; Hagiya, M.; Shimonishi, M.; Nakamura, T.; Shimizu,
submitted to JIPID, March 1991
A;Description: Organization of the human hepatocyte growth fac
                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:M29145; NID:g184041; PIDN:AAA52650.1; PID:g306846 R;Rubin, J.S.; Chan, A.M.L.; Bottaro, D.P.; Burgess, W.H.; Taylor, W.G.; Cech, A.C.; Proc. Natl. Acad. Sci. U.S.A. 88, 415-419, 1991 A;Title: A broad-spectrum human lung fibroblast-derived mitogen is a variant of hepat A;Reference number: A39006; MUID:91110540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:M73239; NID:g337935; PIDN:AAA64239.1; PID:g337936
R;Seki, T.; Thara, I.; Sugimura, A.; Shimonishi, M.; Nishizawa, T.; Asami, O.; Hagi
Biochem. Biophys. Res. Commun. 12, 321-327, 1990
A;Title: Isolation and expression of cDNA for different forms of hepatocyte growth
A;Reference number: A36677; MUID:91025062
A;Accession: B36677
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A,Title: Organization of the human hepatocyte growth factor-encoding
A-Pafarence number: JH0579; MUID:91340155
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                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 1-161,167-728 <RUB>
A; Cross-references: GB: M55379
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A; Residues: 1-161,167-728 <SE4>
A; Cross-references: EMBL:X16323
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                                                                                                       S.; Kondo, J.;
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A; Description: stimulates mitosis of hepatocytes and other cells
A; Note: does not have proteinase activity
C; Superfamily: hepatocyte growth factor; kringle homology; trypsin homology
C; Keywords: alternative splicing; glycoprotein; growth factor; heterodimer; kringle; pyr
F; 131/Domain: signal sequence #status predicted <SIG>
F; 32-494,495-728/Product: hepatocyte growth factor #status experimental <MAT>
F; 32-494/Domain: kringle homology <KR1>
F; 128-206/Domain: kringle homology <KR2>
F; 211-288/Domain: kringle homology <KR2>
F; 395-383/Domain: kringle homology <KR3>
F; 391-469/Domain: kringle homology <KR4>
F; 391-469/Domain: kringle homology <KR4>
F; 395-718/Domain: trypsin homology <KR4>
F; 495-718/Domain: trypsin homology <KR4>
F; 397-4004ified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experiment F; 397-402,566,653/Binding site: carboxylic acid (Gln) (covalent) #status predicted
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A; Residues: 1-288, 'ET' <AIY2>
A; Cross-references: EMBL.X57574; NID:g32083; PIDN:CAA40802.1; PID:g32084
A; Chross-references: EMBL.X57574; NID:g32083; PIDN:CAA40802.1; PID:g32084
R; Shima, N.; Nagao, M.; Ogaki, F.; Tsuda, E.; Murakami, A.; Higashio, K.
Blochem. Blophys. Res. Commun. 180, 1151-1158, 1991
Blochem. Blophys. Res. Commun. 180, 1151-1158, 1991
A; Title: Tumor cytotoxic factor/hepatocyte growth factor from human fibre A; Reference number: 152253; MUID:92062058
A; Accession: 152253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNĀ A; Residues: 1-288 / ET / CHAR> A; Residues: 1-288 / ET / CHAR> A; Cross-references: GB:L02931; NID:g184033; PIDN:AAA52649.1; R; Miyazawa , K.; Kitamura , A.; Naka , D.; Kitamura , N. Eur. J. Biochem. 197, 15-22, 1991 a; Title: An alternatively processed mRNA generated from human A; Reference number: S15443; MUID:91200041
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A;Title: A functional domain in the heavy chain of scatter factor/hepatocyte growth fact A;Reference number: 159214; MUID:93087571
A;Accession: I59214
A;Status: preliminary; translated from GB/EMBL/DDBJ
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A;Residues: 86-91;329-344;356-363,'XX',366-370;425-434;442-447,'X',449-450;543-546,'
A;Residues: 86-91;329-344;356-363,'XX',366-370;425-434;442-447,'X',449-450;543-546,'
R;Nakamura, T.; Nishizawa, T.; Hagiya, M.; Seki, T.; Shimonishi, M.; Sugimura, A.; 1
Nature 342, 440-443, 1989
A;Title: Molecular cloning and expression of human hepatocyte growth factor.
A;Reference number: S06794; MUID:90066676
A;Recession: S06794
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A;Title: Scatter factor: molecular characteristics A;Reference number: A37796; MUID:91035621
A;Accession: A37796
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A;Map position: 7q21.1-7q21.1
A;Introns: 30/1; 85/2; 123/1; 161/2; 209/1; 249/2; 289/1; C;Complex: disulfide-bonded heterodimer of chains derived
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A; Note: the authors translated the codon CAG for residue 727 as Glu
A; Note: part of this sequence, including the amino end of both the a
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A;Residues: 1-31,'HK',34-77,'N',79-292,'V',294-299,'M',301-316,'A',318-335,'K',337-386,
A;Cross-references: EMBL:X16323; NID:g32081; PIDN:CAA34387.1; PID:g32082
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A; Molecule type:
A; Residues: 32-43
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A; Residues: 161-166 <SHI>
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J. Cell Biol. 111, 2097-2108, 1990
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A;Status: preliminary
A;Molecule type: mRMA
A;Residues: 1-728 <TRS>
A;Cross-references: GB:D90102; GB:M32987; NID:g:
A;Cross-references: GB:D90102; GB:M32987; NID:g:
A;Note: the authors translated the codon GAG for
R;Okajima, A; Miyazawa, K; Kitamura, N.
Eur. J. Biochem. 193, 375-381, 1990
A;Title: Primary structure of rat hepatocyte grundlers of the company of the code of the c
hepatocyte growth factor precursor - mouse
N;Alternate names: hepapoietin A; scatter factor
C;Species: Mus musculus (house mouse)
C;Date: 03-Mar-1993 #sequence_revision 26-May-1994 #text_change 16-Jun-2000
C;Accession: JC2117; PC2064; A60185; S43416; S45521; S17173; S10966; I48758;
R;Sasaki, M.; Nishio, M.; Sasaki, T.; Enami, J.
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A; Note: does not have proteinase activity
C; Superfamily: hepatocyte growth factor; kringle homology; trypsin homology
C; Seywords: alternative splicing; glycoprotein; growth factor; heterodimer; kringle;
F; 1-32/Domain: signal sequence #status predicted <SIO>
F; 56-495/Porduct: hepatocyte growth factor #status predicted <MAT>
F; 56-495/Pomain: hepatocyte growth factor alpha chain #status predicted <ACH>
F; 20-207/Domain: kringle homology <KR2>
F; 212-289/Domain: kringle homology <KR3>
F; 306-384/Domain: kringle homology <KR3>
F; 392-470/Domain: kringle homology <KR3>
F; 496-728/Domain: hepatocyte growth factor beta chain #status predicted <BCH>
F; 496-728/Domain: hepatocyte growth factor beta chain #status predicted <BCH>
F; 496-719/Domain: trypsin homology <FRY>
F; 496-719/Domain: trypsin h
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A;Residues: 1-728 <ORA>
A;Cross-references: EMBL:X54400; NID:956353; PIDN:CAA38266.1; PID:94539554
C;Complex: disulfide-bonded heterodimer of chains derived from the same pr
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Pred. No.
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62;
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for residue
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Biochem. Biophys. Res. Commun. 199, 772-779, 1994

A:Title: Identification of mouse manmary fibroblast-derived mammary growth factor as her A:Title: Identification of mouse manmary fibroblast-derived mammary growth factor as her A:Reference number: JC2117; MUID:94183257

A:Accession: JC2117

A:Accession: JC2117

A:Molecule type: mRNA

A:Residues: 1-728 <ASS2>
A:Cross-references: GB:D10212; NID:9220435; PIDN:BAA01064.1; PID:9220436

A:Experimental source: fibroblast, COS-1 cell

A:Molecule type: protein

A:Residues: 496-504 <ASA2>
R:Rosen; E.M.; Meromsky, L.; Setter, E.; Vinter, D.W.; Goldberg, I.D.

Proc. Soc. Exp. Biol. Med. 195, 34-43, 1990

A:Title: Purified scatter factor stimulates epithelial and vascular endothelial cell mig

A:Reference number: A60185; MUID:90377927

A:Accession: A60185; MUID:90377927

A:Accession: A60185; MUID:90377927

A:Coccession: A60185; MUID:9037927

A:Coccession: A60185; MUID:9037927

A:Coccession: A60185; MUID:9037927

A:Cocces
A;Title: Hepatocytes and scatter factor.

A;Tettle: Hepatocytes and scatter factor.

A;Reference number: $10966; MUID:90326152

A;Accession: $10966

A;Status: preliminary

A;Molecule type: protein

A;Residues: 496-507, 'x',509-512,'L',514-516,'X',518-519 <NAT>

R;Plaschke-Schlutter, A.; Behrens, J.; Gherardi, E.; Birchmeier, W.

J. Biol. Chem. 270, 830-836, 1995

A;Title: Characterization of the scatter factor/hepatocyte growth factor gene promoter A;Accession: 148758; MUID:95122532

A;Title: Characterization of the scatter factor/hepatocyte growth factor gene promoter A;Accession: 148758; MUID:95122532

A;Cluber in type: DNA

A;Reference number: I-48758; MUID:9512532

A;Closs-references: EMBL:X81630; NID:9673451; pIDN:CAA57286.1; pID:9673452

C;Complex: disulfide-bonded heterodimer of chains derived from the same precursor C;Function:

A;Description: stimulates mitosis of hepatocytes and other cells

A;Note: does not have proteinase activity

C;Reywords: alternative splicing; glycoprotein; growth factor; heterodimer; kringle homology

C;Reywords: alternative splicing; glycoprotein; growth factor; heterodimer; kringle; p

F;1-32/Domain: signal sequence #status predicted <AMT>

F;56-495,496-728/Product: hepatocyte growth factor #status predicted <ACH>

F;129-207/Domain: kringle homology <KR2>

F;306-384/Domain: kringle homology <KR2>

F;306-384/Domain: kringle homology <KR2>

F;306-384/Domain: kringle homology <KR2>

F;306-470/Domain: kringle homology <KR2>
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A; Reference number: $45521
A; Accession: $45521
A; Accession: $45521
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-563, 'H', 565-728 <LI2>
A; Cross-references: EMBL: X72307
A; Cross-references: EMBL: X72307
B; Coffer, A; Fellows, J; Young, S; Pappin, D.; Rahman, D.
Biochem, J; 278, 35-41, 1991
A; Reference number: $17173; MUID: 91354223
A; Accession: $17173; MUID: 91354223
A; Accession: $17173
A; Accession: $1777; T; 519 <COF>
R; Cofberardi, E; Stoker, M.
Nature 346, 228, 1990
A; Mature 346, 228, 1990
A; Mature 346, 228, 1990
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A;Description: The sequence of A. thaliana T2L5. A;Reference number: 214470
A;Acession: T01956
A;Status. ----
                                                                                                                                                                                                                                                                                                                                                               R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y. M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter Nature 402, 761-768, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                      probable retroelement pol polyprotein [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001 C;Accession: E84589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
E84589
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F;496-719/Domain: trypsin homology <TRX>
F;33/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status F;295,403,569,656/Binding site: carbohydrate (Asn) (covalent) #status predicted F;488-607/Disulfide bonds: #status predicted
                                                                                                                          A; Map position:
C; Superfamily:
                                                                                                                                                                                                          A;Molecule type: DNA
A;Residues: 1-1461 <STO>
A;Cross references: GB:AE002093; NID:g4586028; PIDN:AAD25646.1; GSPDB:GN00139
                                                                                                                                                                                                                                                                                                   A; Reference number: A84420; A; Accession: E84589
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A; Note: T2L5.9
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A;Residues: 1-1244 <GEI>
A;Cross-references: EMBL:AF096371; NID:g3695386; PID:g3695393
A;Experimental source: cultivar Columbia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Accession: T01956
R; Geisel, C.; Smith, A.; Le, submitted to the EMBL Data L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein T2L5.9 - Arabidopsis thaliana C; Species: Arabidopsis thaliana (mouse-ear cress) C; Date: 26-Feb-1999 #sequence_revision 26-Feb-1999
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Best Local Similarity
5; Conserv
                                                                                                                                                                      A; Gene: At2g20460
                                                                                                                                                                                                                                                                                                                         A; Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A; Reference number: A84420; MUID: 20083487
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                                                                                                                                                                                                                                                                                A;Status: preliminary
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Matches 6
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                                                                                                                          retrovirus-related polyprotein
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                                    73.9%;
75.0%;
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Pred. No. 1.1e+02;
2; Mismatches 0;
                                    Score 34;
Pred. No.
DB 2,
1.3e+02;
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                                                         Length 1461;
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Mismatches

0;

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RESULT 14
G69498
calcium-binding protein homolog - Archaeoglobus fulgidus
C:Species: Archaeoglobus fulgidus
C:Species: Archaeoglobus fulgidus
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999
C:Accession: G69498
R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson, Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
Nature 390, 364-370, 1997
A.;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.
A.;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.
A.;Altle: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaed A; Reference number: A69250; MUID:98049343
A.;Accession: G69498
A.;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Residues: 1-313 <KLE>
A;Cross-references: GB:AE000965; GB:AE000782; NID:92669288; PIDN:AAB89260.1; PID:9264854
                                                                                                                                                                                                                                 melanoma antigen MAGE-3 - human

N;Alternate names: MAGE 3 protein

C;Species: Homo sapiens (man)

C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 18-Feb-2000

C;Accession: JC2361; PH1296; I38438

R;Ding, M; Beck, R.J; Keller, C.J.; Fenton, R.G.

Biochem. Biophys. Res. Commun. 202, 549-555, 1994

A;Title: Cloning and analysis of MAGE-1-related genes.
A;Reference number: JC2358; MUID:94311935

A;Accession: JC2361

A;Molecule type: mRNA
A;Praversari, C.; van der Bruggen, P.; Luescher, I.F.; Lurquin, C.; Chomez, P.; Van Pel,
J. Exp. Med. 176, 1453-1457, 1992

A;Title: A nonapeptide encoded by human gene MAGE-1 is recognized on HLA-Al by cytolytic
A;Reference number: PH1294; MUID:93018875

A;Rocession: PH1296

A;Rocession: PH1296

A;Roceule type: DNA
A;Residues: 168-176 <TRA>
A;Rocession: I38438

A;Ccession: I38438

A;Ccession
A;Cross-references: EMBL:U03735; NID:g468825; PIDN:AAA17446.1; PID:g468826 C;Genetics:
A;Gene: MAGE-3
C;Superfamily: tumor associated protein MAGE
F;168-176/Region: HLA-A1 binding #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             γQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 71.7%;
Best Local Similarity 62.5%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       272 IEIGHVYI 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    544 RIGNLYVL 551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 VRIGHLYI 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 RIGHLYIL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 33; DB 2; Length 313;
Pred. No. 39;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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Query Match
Best Local Similarity 100.0%; Pred. No. 39;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps

Qy 3 IGHLYI 8
Litit
Db 172 IGHLYI 177
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Search completed: June 20, 2001, 14:04:33 Job time: 80 sec